



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 123519

**TO:** Christopher Yaen  
**Location:** REM/3A20/3C18  
**Art Unit:** 1642  
June 4, 2004

**Case Serial Number:** 09/700770

**From:** P. Sheppard  
**Location:** Remsen Building  
**Phone:** (571) 272-2529

**[sheppard@uspto.gov](mailto:sheppard@uspto.gov)**

Search Notes

**From:** Yaen, Christopher  
**Sent:** Wednesday, June 02, 2004 10:33 AM  
**To:** STIC-Biotech/ChemLib  
**Subject:** 09700770

could you please search seq id 7, 8, and 9

thanks

Chris

Christopher Yaen  
US Patent Office  
Art Unit 1642  
571-272-0838  
REM 3A20  
REM 3C18

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: \_\_\_\_\_  
Date Completed: \_\_\_\_\_  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: \_\_\_\_\_  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: \_\_\_\_\_  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

Result No.	Score	Query	Match	Length	DB	ID	Description
1	225	44.8	94	11	Q8CJC6		Q8cjc6 mus musculus
2	88	17.5	255	16	Q82LN6		Q82ln6 streptomyces
3	83.5	16.6	281	16	Q8FST3		Q8fst3 corynebacterium
4	82.5	16.4	247	16	Q9K3G4		Q9k3g4 streptomyces
5	82.5	16.4	694	16	Q98CR1		Q98cr1 rhizobium
6	81	16.1	496	10	Q9SUB3		Q9sub3 arrobacter
7	80	15.9	148	16	Q8XW23		Q8xw23 ralstonia
8	79	15.7	136	16	Q82R50		Q82r50 streptomyces
9	77.8	15.4	229	16	Q7WU66		Q7wu66 bordetella
10	77.5	15.4	229	16	Q7WA34		Q7wa34 bordetella
11	77.5	15.4	229	16	Q7VVA1		Q7vva1 bordetella
12	77	15.4	601	16	Q86691		Q86691 streptomyces
13	77	15.3	453	17	Q8THL0		Q8thl0 methanobacter
14	76	15.1	355	16	Q8UA14		Q8ua14 acrobacter
15	76	15.1	699	16	Q9ABLO		Q9abl0 caulobacter
16	76	15.1	889	16	Q8G4X4		Q8g4x4 bifidobacter

Title:	US-09-700-770-9	Run on:	June 2, 2004, 20:07:29 ; Search time 16.5872 Seconds (without alignments)
Perfect score:	502	Sequence:	1 MKLAALLGICVALSSCSAAA.....QAVGAVKALKALLGALITVFG 104
Scoring table:	BLOSUM62	Gapop 10.0 , Gapext 0.5	
Searched:	1017041 seqs, 315518202 residues		
Total number of hits satisfying chosen parameters:	1017041		
Minimum DB seq length: 0			
Maximum DB seq length: 2000000000			
Post-processing: Minimum Match 0%			
Maximum Match 100%			
Database :	SPTREMBL 25:*		
1:	sp_archea:*		
2:	sp_bacteria:*		
3:	sp_fungi:*		
4:	sp_human:*		
5:	sp_invertebrate:*		
6:	sp_mammal:*		
7:	sp_mhc:*		
8:	sp_organelle:*		
9:	sp_phage:*		
10:	sp_plant:*		
11:	sp_rat:*		
12:	sp_virus:*		
13:	sp_vertebrate:*		
14:	sp_unclassified:*		
15:	sp_virus:*		
16:	sp_bacteria:*		
17:	sp_archeap:*		

17	75.5	15.0	459	16	Q9F2L6		
18	75.5	15.0	496	16	Q8G3S5		
19	75.5	15.0	544	17	Q9F3S2		
20	75.5	15.0	667	16	Q8XRM8		
21	75	14.9	299	16	Q89T3		
22	75	14.9	355	2	Q8RPKS		
23	75	14.9	370	16	Q89K46		
24	75	14.9	463	11	Q8C313		
25	74	14.7	611	16	Q8L0K1		
26	73.5	14.6	119	5	Q86D11		
27	73.5	14.6	331	17	Q9HN19		
28	73.5	14.6	358	16	Q8NC28		
29	73.5	14.6	389	16	Q8E001		
30	73	14.6	148	5	Q9GFB5		
31	73	14.5	317	16	Q9BD48		
32	73	14.5	429	16	Q825M1		
33	73	14.5	502	16	Q915I2		
34	73	14.5	542	10	Q86YAI		
35	73	14.5	584	16	Q9AAR5		
36	73	14.5	620	16	Q7WL37		
37	73	14.5	620	16	Q7WQ0		
38	73	14.5	620	16	Q7VVB7		
39	73	14.5	1279	5	Q46099		
40	72.5	14.4	240	2	Q84CV5		
41	72.5	14.4	373	5	Q7TW1		
42	72.5	14.4	384	16	Q88KE1		
43	72.5	14.4	421	2	Q93177		
44	72.5	14.4	482	5	Q9BHf9		
45	72.5	14.4	616	16	Q7W2M5		

## ALIGNMENTS

RESULT 1	Q8CJC6	PRELIMINARY;	PRT;	94 AA.
ID	Q8CJC6			
AC	Q8CJC6;			
DT	01-MAR-2003	(TREMBLref).	23, Created)	
DT	01-MAR-2003	(TREMBLref).	23, Last sequence update)	
DT	01-JUN-2003	(TREMBLref).	24, Last annotation update)	
DE	UGRP2	type B.		
GN	SCGB3A1			
OS	Mus musculus (Mouse)			
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
RN	[1] NCBITaxonID=10090;			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=2232674; PubMed=12438750;			
RA	Nini T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodsai A., Zimonic D.B., Keck Wargner C.L., Popescu N.C., Kimura S.; "Cloning, expression, and chromosomal localization of the mouse gene (Scgb3a1, alias Ugrp2) that encodes a member of the novel uteroglobin-related protein gene family."			
RL	Cytogenet. Genome Res. 97:120-127 (2002).			
DR	EMBL; AF313457; AAC62328.1; -.			
DR	MGI: MGI:1915912; Scgb3a1.			
SEQNCE	94 AA;	9578 MW;	7C84B908A6365B59 CRC64;	
Query Match	44	8%	Score 225;	
Best Local Similarity	57.3%		Pred. No. 2e-13;	
Matches	51;	Conservative	14;	MS matches 20;
DR	MGD: MGI:1915912; Scgb3a1.			
DR	NCBI_TAXID=10090;			
DR	SGP: Q9AVGAKAALKAILGALITVFG 104			
DR	QKCVAEIGPQAVGAKAALKAILGALITVFG 104			
DR	RKCVTBLGPVERGVAA--KSLLGVLTMF 94			

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	225	44.8	94	11	Q8CJC6		Q8cjc6 mus musculus
2	88	17.5	255	16	Q82LN6		Q82ln6 streptomyce
3	83.5	16.6	281	16	Q8FST3		Q8fst3 corynebacte
4	82.5	16.4	247	16	Q9K3G4		Q9k3g4 streptomyce
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6	81	16.1	496	10	Q9SUB3		Q9sub3 arrobacter
7	80	15.9	148	16	Q8XW23		Q8xw23 ralstonia
8	79	15.7	136	16	Q82R50		Q82r50 streptomyce
9	77.8	15.4	229	16	Q7WU66		Q7wu66 bordetella
10	77.5	15.4	229	16	Q7WA34		Q7wa34 bordetella
11	77.5	15.4	229	16	Q7VVA1		Q7vva1 bordetella
12	77	15.4	601	16	Q86691		Q86691 streptomyce
13	77	15.3	453	17	Q8THL0		Q8thl0 methanobacter
14	76	15.1	355	16	Q8UA14		Q8ua14 acrobacter
15	76	15.1	699	16	Q9ABLO		Q9abl0 caulobacter
16	76	15.1	889	16	Q8G4X4		Q8g4x4 bifidobacte

RESULT 2		RC STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;
QB2LN6 PRELIMINARY;	PRT;	255 AA.
AC	RA Kawaabayasi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,	
ID	RA Ikeda K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,	
QB2LN6	RA Usuda Y., Sugimoto S.,	
DT 01-JUN-2003 (TREMBLrel. 24, Created)	RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";	
DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)	Submitted (MAY-2003) to the EMBL/GenBank/DBU databases.	
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)	DR EMBL; AP005215; BAC17109.1;	
DE Putative methionine aminopeptidase.	DR Conserved hypothetical protein.	
GN	KW Hypothetical protein; Complete proteome.	
NCBI_TaxID=33903;	SQ SEQUENCE 281 AA; 21988 MW; 3143B99C35048C2D CRC64;	
RN	Query Match Score 83.5; DB 16; Length 281;	
RP SEQUENCE FROM N.A.	Best Local Similarity 30.1%; Pred. No. 7.7;	
RC STRAIN=YA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	Matches 40; Conservative 9; Mismatches 45; Indels 39; Gaps 7;	
RX MEDLINE=21477403; PubMed=11572948;	Q9K3G4 PRELIMINARY; PRT;	
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,	106 LAGFLGLCIGLNLRAAGAPMADAMDHAAHTTGTSAGHTVTAARRVRSQGGAVL 165	
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osoneo T.,	48 ANP -----LGTL-----NELLKLSSLLGIPVNHLIEGS----OKCVAAEL-GPOAV 87	
RA Kiruchi H., Shiba T., Sakaki Y., Hattori M.,	166 IDPTMDLORLIGTIVWEVSERHGFPLVRLDQL---KHLRQAERHRDASAAGLQGPAT 221	
RT "Genome sequence of an industrial microorganism Streptomyces avermitilis: deducing the ability of producing secondary metabolites."	Qy 3 LANLICCV-----ALSCSSAAAELVGSAKPVQGPVALESAAR-----AGAGTL 47	
RT Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).	Db 106 LAGFLGLCIGLNLRAAGAPMADAMDHAAHTTGTSAGHTVTAARRVRSQGGAVL 165	
RN	Db 48 ANP -----LGTL-----NELLKLSSLLGIPVNHLIEGS----OKCVAAEL-GPOAV 87	
RP SEQUENCE FROM N.A.	Db 166 IDPTMDLORLIGTIVWEVSERHGFPLVRLDQL---KHLRQAERHRDASAAGLQGPAT 221	
RC STRAIN=YA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;	Qy 88 GAVKALKALIGAL 100	
RX MEDLINE=21477403; PubMed=11572948;	Db 222 AVIALLPLAGVL 234	
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,	RESULT 4	
RA Sakaki Y., Hattori M., Omura S.,	Q9K3G4 PRELIMINARY; PRT;	
RT "Complete genome sequence and comparative analysis of the industrial microorganism Streptomyces avermitilis".	ID Q9K3G4; AC Q9K3G4; DT 01-OCT-2000 (TREMBLrel. 15, Created)	
RL RIBOtechnol. 21:526-531 (2003).	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)	
DR EMBL; AP005029; BA69685.1;	DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)	
DR GO; GO:0004239; F: methionine aminopeptidase activity; IEA.	GN SC01277 OR 2SGG18_24.	
DR GO; GO:0006508; P: proteolysis; I: peptidolysis; IEA.	OS Streptomyces coelicolor.	
DR InterPro; IPR00994; Peptidases_M24.	OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetes.	
DR InterPro; IPR002467; Pept_M24A_MAPI.	OC Streptomyces; Streptomyctaceae; Streptomyces.	
DR Pfam; PF00557; Peptidase_M24_1.	NCBI_TaxID=19302; OX	
DR PRINTS; PR0059; MAPEPTIDASE.	RN	
DR TIGRFAMS; TIGR00500; met_peptidase.	RP SEQUENCE FROM N.A.	
DR AminoPeptidase; Complete_Proteome.	RC STRAIN=A3(2) / ML45; MEDLINE=21956410; PubMed=12000953; RX	
KW SEQUENCE 255 AA; 26727 MW; 0C41CD3010F855A3 CRC64;	RA Bentley S.D., Chater K.F., Cerdeno-Tarrazza A.-M., Challis G.L., RA Thomson N.R., James K.D., Harris D.B., Quail M.A., Kieser H., RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howe S., RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S., RA Rabbinowitsch E., Rajandream M.A., Rutherford K., Buttner S., RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K., RA Warren T., Wierzorek A., Woodward J., Barrell B.G., Parkhill J., RA Hopwood D.A.; RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3(2)." RL Nature 417:141-147 (2002).	
SQ DR EMBL; AL93910B; CAB99157.1; -.	DR EMBL; AL93910B; CAB99157.1; -.	
Query Match Score 82.5; DB 16; Length 247;	KW Hypothetical protein; Complete proteome.	
Best Local Similarity 31.8%; Pred. No. 8.3;	SQ SEQUENCE 247 AA; 22950 MW; E32ABD76146881B CRC64;	
Matches 34; Conservative 10; Mismatches 40; Indels 23; Gaps 5;	Query Match Score 82.5; DB 16; Length 247;	
Qy 17 SAAAPFLVGSAKP-----VAQPVAALESAAFG-----AGTMLNPLGTL-----NPLKL 59	Best Local Similarity 31.8%; Pred. No. 8.3;	
Db 61 NALAAAGAVNPATLAGVTNPLAALGGIGAGNPLAGLAGAGPLGNTAGAAONPLAA 120	Matches 34; Conservative 10; Mismatches 40; Indels 23; Gaps 5;	
Qy 60 LLSSL--GIPVNHLIGSQKVCVABLGQAVYA 89	Qy 17 SAAAPFLVGSAKP-----VAQPVAALESAAFG-----AGTMLNPLGTL-----NPLKL 59	
Db 121 LTGAAAGGNPLAAALGGAGNPLAALG-----GAANPLAAVGAAAGALG 163	Db 61 NALAAAGAVNPATLAGVTNPLAALGGIGAGNPLAGLAGAGPLGNTAGAAONPLAA 120	
RESULT 3	OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.	
Q8FST3 PRELIMINARY;	OC Corynebacter; Actinobacteria; Actinomycetaceae.	
ID Q8FST3	[1]	
AC Q8FST3;	RN SEQUENCE FROM N.A.	
DT 01-MAR-2003 (TREMBLrel. 23, Created)	RP	
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)		
DE Conserved hypothetical protein.		
GN CB0293		
OS Corynebacterium efficiens.		
OC Bacteria; Actinobacteria; Actinomycetaceae; Actinomycetes.		
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.		
RN		



DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DE Putative invasion protein.  
GN SAV294  
CS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Streptomyctaceae; Streptomyces.  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; Published=1572948;  
RA Omura S., Ikeda H., Ishii J., Hanamoto A., Takahashi C.,  
Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osono T.,  
RA Shikino H., Shiba T., Sakai Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
avermitilis: deducing the ability of producing secondary  
metabolites."  
RT RT

Query Match 15.3%; Score 77; DB 17; Length 453;  
Best Local Similarity 27.8%; Pred. No. 52; Gaps 4;  
Matches 30; Conservative 20; Missmatches 34; Indels 24; Gaps 4;

QY 11 VALCSSLAAAFLYGSAKPVQAQVALESAABAGTIANPLGTNPKLSSLGIPVNH 70  
Db 102 MAAKAGADVAILGSADD-STILDALRASAHKGYTRMADLISAPEPIKRAVDLEALGVDY 160

QY 67 -----PWNHLEGSKVCAVHL---GPQAVGAVALKKA 95  
Db 161 INVHVIGDQQMYGKDPISTIMESEKVSYQLAVAGGLDAEGRACKVA 208

RESULT 14  
Q8IAI4 PRELIMINARY; PRT; 355 AA.  
AC Q8IAI4;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)  
DB ABC transporter, membrane spanning protein.  
GN ATU3389 OR ACR\_L\_2865.  
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.  
OX NCBI\_TAXID=176299;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21608550; PubMed=11743193;  
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,  
Okura Y.K., Zhou Y.Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,  
Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Boyce D. S.,  
Chapman P., Clendinning J., Deatherage G., Gillett W., Grant C.,  
Kutayvin F., Levy R., Li M.-J., McClelland E., Palmeri A.,  
Raymond C., Rouse G., Saemphumchak C., Wu Z., Romero P., Gordon D.,  
Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,  
Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,  
Nester E.W.;  
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens  
C58.";  
RT Science 294:2317-2323 (2001).  
RN RP SEQUENCE FROM N.A.  
RX MEDLINE=1160551; PubMed=11743194;  
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,  
Houmille K., Gordon J., Vaudin M., Dartchouk O., Epp A., Liu F.,  
Wollam C., Allinger M., Doughty D., Scott C., Happas C., Markelz B.,  
Cielo C., Slater S.;  
RT "Genome sequence of the plant pathogen and biotechnology agent  
Agrobacterium tumefaciens C58.";  
.RX Science 294:2323-2328 (2001).  
DR EMBL; A0009269; AAL44202.1;  
DR EMBL; A0008343; AAK90001.1;  
PTR; AD2973; ADD2973.  
DR GO:0016020; C:membrane; IEA.

Query Match 15.1%; Score 76; DB 16; Length 699;  
Best Local Similarity 30.5%; Pred. No. 1e+02;  
Matches 32; Conservative 18; Missmatches 37; Indels 18; Gaps 5;

QY 11 VALCSSLAAAFLYGSAKPVQAQVALESAABAGTIANPLGTNPKLSSLGIPVNH 70  
Db 144 VQALASAASFAGVAGLPLATAMA-----PLAQMPVVIAGSVAGLIG 189

QY 71 LIEGSKQKVCAVHLQPVAV----GAYKALKALLGALTVEFG 104  
Db 190 AV-AARAGGAPVGVPAVAVVLLGAAMALTAVGAL--FG 226

Query Match 15.1%; Score 77.5; DB 16; Length 229;  
Best Local Similarity 32.0%; Pred. No. 22;  
Matches 32; Conservative 15; Missmatches 30; Indels 23; Gaps 4;

QY 11 VALCSSLAAAFLYGSAKPVQAQVALESAABAGTIANPLGTNPKLSSLGIPVNH 70  
Db 24 RILLVLGLPLACFSMADMALGMPARYTSEVLA-----TIADPAAVGNQLRVRV 73

QY 62 SSQJLIPVNHL-----IEGSQKCVW-----ELGPOAVGAVKALKALLGALTVEFG 103  
Db 74 WD1RIMPALMATTVGASLSVAGRMOTILSNPLASPTFTLIGSAAASFGAAALVGGVIAF 133

RESULT 15  
Q9A8L0 PRELIMINARY; PRT; 699 AA.  
ID Q9A8L0  
AC Q9A8L0;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
DB Thio:disulfide interchange protein, putative.  
GN CC2217.

Q9A8L0 SEQUENCE FROM N.A.  
RC STPATIN-NCTC 19089 / CB115;  
RX MEDLINE=21173698; PubMed=11259647;  
RA Nieerman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Poocca I., Nelson W.C., Nelson N.D., Stephens C., Phadke N.D., Ely B.,  
RA Deoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
RA Utterback T., Tran K., Wolf J., Vamathevan J., Brmolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of Caulobacter crescentus.";  
RL PRC Natl. Acad. Sci. U.S.A. 98:4136-4141 (2001).  
DR EMBL; AE005636; AAK22204.1; -.  
DR PTOR; CC2217;  
DR DR GO:00016020; C:membrane; IEA.  
DR GO:0005618; P:cytochrome biogenesis; IEA.  
DR InterPro; IPR003834; Cytotoch TM  
DR InterPro; IPR006663; Thioredox\_dom2.  
DR Pfam; PF02653; DbdD; 1.  
KW Complete proteome:  
SQ SEQUENCE 699 AA; 70749 MW; 652319CA7E88B943 CRC64;

Query Match 15.1%; Score 76; DB 16; Length 699;  
Best Local Similarity 30.5%; Pred. No. 1e+02;  
Matches 32; Conservative 18; Missmatches 37; Indels 18; Gaps 5;

QY 3 LARLGLTVALLSOSAANFLVSSAKPVAQPYVALESAAEAGTTLANPLGTNPKLSSLGIPVNH 61  
Db 545 VSMIGLGLAVVGAALAAASLASKP-----QCKCVAAELGFQAVGAVKALKAL 97

QY 62 SSQJLIPVNHLGS-----PVAEEASTPSGPGLTAE---AWSPEVKVQAL 598  
Db 599 QERGPRP----LVDFIAAMCVTCVNEYKVALSGPFAKNAVNL 641

Result No.	Score	Query Match %	Length	DB ID	Description
1	497	99.0	104	1 UGR2_HUMAN	096rx1 homo sapien
2	250	49.8	104	1 UGR2_MOUSE	Q92qd7 mus musculu
3	160	31.9	93	1 UGR1_HUMAN	Q96p11 homo sapien
4	135	26.9	139	1 UGR1_MOUSE	Q92oh1 mus musculu
5	83	16.5	1327	1 TNKL_HUMAN	Q95271 homo sapien
6	77	15.3	335	1 TRD2_STRCO	[2] Q9zlw9 helicobacte
7	76	15.1	732	1 COPA_HELICE	Q32619 helicobacte
8	75	14.9	362	1 MDCL_HUMAN	Q9nkh5 homo sapien
9	75	14.9	362	1 MDCL_MOUSE	Q9er88 mus musculu
10	74	14.7	779	1 SNIL_MOUSE	Q60670 mus musculu
11	73	14.6	626	1 DXS_WIGBR	Q84357 wigglewort
12	73.5	14.6	776	1 SNIL_RAT	Q9f412 ratmus norv
13	73.5	14.6	882	1 SYA_THETH	P74941 thermus the
14	72	14.3	397	1 SUCC_AGR75	Q8k660 agrobacteri
15	71	14.1	428	1 FXB2_MOUSE	Q67733 mus musculu
16	71	14.1	480	1 DNAA_RHIME	P36590 rhizobium m
17	69	13.7	124	1 RL7_RALSO	Q8kuz7 ralstonia s
18	68	13.6	377	1 PRO_BIFLO	Q89479 bifidobacte
19	68	13.5	334	1 FEPD_ECOLI	P23676 escherichia
20	68	13.5	569	1 SILF_MOUSE	Q92og3 mus musculu
21	67.5	13.4	2035	1 Y233_HUMAN	Q92op8 homo sapien
22	67	13.3	351	1 GCP_MYCLE	P37769 mycobacteri
23	67	13.3	464	1 FUMC_PSEM	Q885v0 pseudomonas
24	66	13.2	341	1 TAZR_RAT	P34978 ratmus norv
25	66.5	13.2	465	1 FXD1_HUMAN	Q16676 homo sapien
26	66	13.1	118	1 NLTD_BRADL	Q43304 brasiliaca ol
27	66	13.1	121	1 MP70_MYCOL	Q46514 mycobacteri
28	66	13.1	239	1 CLRC_IDEDE	P60000 ideonella d
29	66	13.1	527	1 PTB_MOUSE	P17225 mus musculu
30	66	13.1	545	1 LEU1_PRMM	Q77av5 prochloroco
31	66	13.1	585	1 NUP1_RAT	P70581 rattus norv
32	65.5	13.0	257	1 EUTC_RHOER	Q57982 rhodococcus
33	65.5	13.0	336	1 COBT_RHIL0	Q98kn9 rhizobium l

ALIGNMENTS					
RESULT :-					
UGR2_HUMAN	STANDARD;				
ID UGR2_HUMAN	Q96P10;				
AC Q96P11; Q96P10;					
DT 28-FEB-2003 (Rel. 41, Created)					
DT 28-FEB-2003 (Rel. 41, Last sequence update)					
DT 28-FEB-2003 (Rel. 41, Last annotation update)					
DE "HIN-1", a putative cytoline precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).					
GN SCB3A1 OR UGRP2 OR HIN1.					
NCBI_TaxID=9606;					
RN [1]					
RP SEQUENCE FROM N.A.					
RX MEDLINE:21390515; PubMed=11481438;					
RA Krop I.E., Sgròi D., Porter D.A., Lunetta K.L., Levangie R., Seth P., Kaslin C.M., Rhei E., Rosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyak K.;					
RA RT "HIN-1", a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells.";					
RA Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801 (2001).					
RL [2]					
RN RN					
RP SEQUENCE FROM N.A.					
RX MEDLINE:2153178; PubMed=11682631;					
RA Niimi T., Keek-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;					
RA RT "URP1, a uteroglobin/clarke cell secretory protein-related protein, a lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";					
RT RT Mol. Endocrinol. 15:2031-2036 (2001).					
CC CC -1. FUNCTION: Potential growth inhibitory cytokine.					
CC CC -1. SUBCELLULAR LOCATION: Secreted.					
CC CC -1. TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in breast cancer cell lines.					
CC CC -1. SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.					
CC CC -1. -					
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CC BMBL: AY040564; AAK82942.1; -.					
CC BMBL: AF313458; AAL26217.1; -.					
CC Gerew, HGNC:18384; SCB3A1. -.					
CC MIN; 606500; -.					
CC DR GO; GO:00050516; C:extracellular; NAS.					
CC DR GO; GO:000515; F:cytokine activity; NAS.					
CC DR GO; GO:00030108; P:negative regulation of cell growth; NAS.					
CC DR GO; GO:0042127; P:regulation of cell proliferation; NAS.					
KW KW Cytochrome; Signal.					
FT SIGNAL ; Signal 1 20 POTENTIAL.					

FT	CHAIN	21	104	UTEROGLOBIN-RELATED PROTEIN 2.	
FT	CONFLICT	19	19	R -> (IN REF. 2).	
SQ	SEQUENCE	104 AA;	10185 MW;	108373C8FAE8015 CRC64;	
Query Match		99.0%;	Score 497; DB 1;	Length 104;	
Best Local Similarity		99.0%;	Pred. No. 7.2e-38;		
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;					
Qy	1 MKLAAALLGLCVALSCSSAAAFLVGSAAKPAQVAALESAAEAGCTIANTPLGTLNPKLL 60				
Db	1 MKLAAALLGLCVALSCSSAAAFLVGSAAKPAQVAALESAAEAGCTIANTPLGTLNPKLL 60				
Qy	61 LSSLGIPYNHLLEGSOQCCVAELGPQAVAKALKALGALTYFG 104				
Db	61 LSSLGIPYNHLLEGSOQCCVAELGPQAVAKALKALGALTYFG 104				
RESULT 2					
ID	UGR2_MOUSE	STANDARD;	PRT;	104 AA.	
AC	Q920D7;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DS	Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in				
DE	normal-1) (Secretoglobin family 3A member 1).				
GN	SCGB3A1 OR UGRP2 OR HIN1.				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
CC	Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Mus;				
RN	[1] -TaxID=10099;				
RP	SEQUENCE FROM N.A.				
RA	MBID=21396515; PubMed=11481438;				
RA	Krop T.E., Sgricci D., Porter D.A., Lunetta K.L., Levangie R., Seth P.,				
RA	Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z.,				
RA	Rau D., Razumovic J., Polak K.				
RA	"HIN-1", a putative cytokine highly expressed in normal but not				
RA	cancerous mammary epithelial cells." Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).				
RA	[2]				
RP	SEQUENCE FROM N.A.				
RA	MBID=21539178; PubMed=11682631;				
RA	Nimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,				
RA	Kimura S.				
RA	"UGRP1, a uteroglobin/clara cell secretory protein-related protein, is				
RA	a novel lung-enriched downstream target gene for the T/EBP/NKX2.1				
RA	homeodomain transcription factor". Mol. Endocrinol. 15:2021-2036(2001).				
RA	-!- FUNCTION: Potential growth inhibitory cytokine.				
RA	-!- SUBCELLULAR LOCATION: Secreted (By similarity).				
RA	-!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
CC	modified and this statement is not removed. Usage by and for commercial				
CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).				
CC	DR EMBL: AP13456; AAL26216.; -.				
CC	DR MGD; MGI:1915912; Scgb3a1.				
KW	Cytokine; Signal.				
PT	SIGNAL 1 21 POTENTIAL.				
PT	CHAIN 22 104 UTEROGLOBIN-RELATED PROTEIN 2.				
SQ	SEQUENCE 104 AA; 10591 MW; D62FFB601FB57A6 CRC64;				
Query Match	49.8%; Score 250; DB 1; Length 104;				
Best Local Similarity	57.0%; Pred. No. 8.2e-16;				
Matches 61; Conservative 14; Mismatches 26; Indels 6; Gaps 4;					
Qy	1 MKLAAALLGLCVALSCSSAAAFLVGS-AKPVQAQVAALESAEAAGCTIANTPLGTLNPL 57				

FT SIGNAL	1	21	POTENTIAL.		FT VARSPPLIC	1.07	139	VSVFLPLMICAYPPDSKQQTFAFFTERVFEQSKL -> EALS
FT CHAIN	22	93 AA:	10161 MW;	FBDDBERCBFB3:3718 CRC64;	FT FT			HLV (in isoform B).
SQ SEQUENCE	93 AA:				FT FT			/FTId=VSP_006726-
Query Match	31.9%	Score 160;	DB 1;	Length 93;	FT FT			VIIICSY -> EASHLV (in isoform A).
Best Local Similarity	43.6%	Pred. No. 8..1e-08;			FT FT			/FTId=VSP_006727-
Matches 44;	Conservative	9;	Mismatches 38;	Indels 10;	FT FT			Missing (in isoform A).
QY	1 MKLAAALLGLCVALS-CS-SAAAFLVGSAKPVAAQPVAALESAAEAGAGTIANPLGTINPLKL 59				FT FT			/FTId=VSP_006728-
Db	1 MKLVTIIFLVITLISLSSYSSATAFLINKVLPVVDKLAPL-----PLDNILPFMDPLKL 51				FT SQ	SEQUENCE	139 AA;	15431 MW;
QY	60 LSSSLGIPVNHLIIGSQKCVAAELGPOAVGAVKALKALGAL 100				FT FT			8A2FB080B41B365E4 CRC64;
Db	52 LLKTGIGSYVHLVEGRKCVNELGEASEAVKCKLLEALSHL 92				Qy	1 MKLALLGLGIVCALGCCSSAAAFLVGSAKPVAAQPVAALESAAEAGAGTIANPLGTINPLKL 60		
RESULT 4	UGR1_MOUSE	STANDARD;	PRT;	139 AA.	Qy	1 MKLVTIIFLVITLISLSSYSSATAFLINKVLPVVDKLAPL-----PLDNILPFMDPLKL 61		
ID UGR1_MOUSE	Q920H1; Q920H2; Q920H3;				Db	51 LKTAGISVSEHLVTSURKCVDLGEBASEAVKCLLIVI 87		
AC Q920H1					Qy	61 LSSSLGIPVNHLIIGSQKCVAAELGPOAVGAVKALKALI 97		
DT 28-FEB-2003	(Rel. 41. Created)				Db	51 LKTAGISVSEHLVTSURKCVDLGEBASEAVKCLLIVI 87		
DT 28-FEB-2003	(Rel. 41. Last sequence update)							
DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A member 2).								
GN SCGB3A2 OR UGRP1.								
OS Mus musculus (Mouse).								
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. [1]								
OC								
OX TAXID=10090;								
RN RP								
SEQUENCE FROM N.A. (ISOFORMS A; B AND C).								
RC TISSUE=Lung;								
RC MEDLINE=21539178; PubMed=11682631;								
RA Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., RA Smith S., Giriati I., Schmitt A., de Lange T.;								
RA Kimura S.;								
RT "UGR1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor.";								
RT Mol. Endocrinol. 15:2021-2036(2001).								
CC -- SUBUNIT: Homodimer.								
CC -- ALTERNATIVE LOCATION: Secreted.								
CC Event-Alternative splicing; Named isoforms=3;								
CC Name=C;								
CC IsoId=Q920H1-1; Sequence=Displayed;								
CC Name=A;								
CC IsoId=Q920H1-2; Sequence=VSP_006727; VSP_006728;								
CC Name=B;								
CC IsoId=Q920H1-3; Sequence=VSP_006726;								
CC -- TISSUE SPECIFICITY: Belongs to the uteroglobin family. UGTP subfamily.								
CC -- SIMILARITY: Belongs to the uteroglobin family. UGTP subfamily.								
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CC EMBL; AF214959; AF25708; AF25709; AF25710; AF25711;								
CC EMBL; AF214960; AF25709; AF25710; AF25711;								
CC MGD; MGI:2153470; Scgb3a2;								
CC GO; GO:0005515; F:protein binding; IDA.								
CC InterPro; IPR006038; uteroglobin_supF.								
CC Pfn1; PF0099; Uteroglobin; 1.								
CC KWF; Alternative splicing.								
CC SIGNAL; Alternative splicing.								
FT SIGNAL	1	21	POTENTIAL.					
FT CHAIN	22	139	UTEROGLOBIN-RELATED PROTEIN 1.					

-!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and with juxtanuclear SLC2A4/Glut4 vesicles. A minor proportion is also found at nuclear pore complexes and around the pericentriolar matrix of mitotic centromeres. During interphase, a small fraction of TNKS is found in the nucleus, associated with TRFL.

-!- ALTERNATIVE PRODUCTS:

-!- Event=Alternative splicing; Named isoforms=2;

Name=1;

CC IsoId=095271-1; Sequence=Displayed;

CC IsoId=095271-2; Sequence=VSP 004538; VSP 004539;

CC Note=No experimental confirmation available;

CC TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.

CC PTM: Upon insulin-stimulation, phosphorylated on serine residues by MAPK kinases.

CC PTM: ADP-ribosylated (-auto).

CC SIMILARITY: Belongs to the PARP family.

CC SIMILARITY: Contains 15 ANK repeats.

CC SIMILARITY: Contains 11 sterile alpha motif (SAM) domain.

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CC GeneName: HGNC:11941; TNKS.

CC MIM: 603303; -;

DR GO: GO:0000781; C:chromosome, telomeric region; IDA.

DR GO: GO:0003950; F:NAD ADP ribosyltransferase activity; IDA.

DR GO: GO:0005515; F:protein binding; IPI.

DR GO: GO:0007004; P:telomerase-dependent telomere maintenance; NAS.

DR Intertro; IPR001110; ANK.

DR Intertr; IPR001660; SAM.

DR Pfam; PF00023; ank; 19.

DR Pfam; PF00536; SAM; 1.

PRINTS; PRO1415; ANKYRIN.

SMART; SM00248; ANK; 17.

SMART; SM00454; SAM; 1.

PROSITE; PS50088; ANK REPEAT; 15.

PROSITE; PS50291; ANK REP REGION; 1.

PROSITE; PS50105; SAM DOMAIN; 1.

KW Transerase; Glycosyltransferase; NAD; Golgi stack; Telomere; Nuclear protein; Repeat; ANK repeat; ADP-ribosylation; RNW

RW Phosphorylation; Alternative splicing.

FT REPEAT 215 247 ANK 1.

FT REPEAT 248 280 ANK 2.

FT REPEAT 281 313 ANK 3.

FT REPEAT 368 400 ANK 4.

FT REPEAT 401 433 ANK 5.

FT REPEAT 434 466 ANK 6.

FT REPEAT 521 556 ANK 7.

FT REPEAT 557 589 ANK 8.

FT REPEAT 590 622 ANK 9.

FT REPEAT 683 715 ANK 10.

FT REPEAT 716 748 ANK 11.

FT REPEAT 747 781 ANK 12.

FT REPEAT 836 868 ANK 13.

FT REPEAT 869 901 ANK 14.

FT REPEAT 902 934 ANK 15.

FT DOMAIN 1030 1089 SAM.

FT DOMAIN 1176 1327 PARP.

FT DOMAIN 9 14 POLY-HIS.

FT DOMAIN 27 34 POLY-PRO.

FT DOMAIN 128 134 POLY-SER.

FT DOMAIN 145 145 POLY-SER.

FT VARSPLIC 641 643 EST-> GHS (in isoform 2). /FTID=VSP 004538.

FT VARSPLIC 644 1327 Missing (in isoform 2). /FTID=VSP 004539.

FT MUTAGEN 1184 1184 H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.

FT MUTAGEN 1291 1291 B->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1184.

SQ SEQUENCE 1327 AA; 142010 MW; E14DE95C710B957 CRC64;

Query Match 16.5%; Score 83; Length 1327;

Best Local Similarity 30.5%; Pred No. 6.5;

Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

Qy 15 CSBAAAFLVSSAKPYAQPVAALESA-----EAGAGTLANPLGLTNPKLULSSIGIYN 69

Db 90 CSTSITCTVAAAPV-PAVTSSTAGVADPNPGSNNNPSSSSPSSSPSGS 148

Qy 70 HLIESQ-----KCVAELGPQAVGAYKALKALLGAL 100

Db 149 SIAESPEAGGSSTAPLGPGRAAGPTGVAVSGAL 183

RESULT 6

TRD2\_STRCO ID TRD2\_STRCO STANDARD; PRT; 335 AA.

AC 092498; AC 092498; (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 30-MAY-2000 (Rel. 39, Last annotation update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DB Anthranilate phosphoribosyltransferase 2 (EC 2.4.2.18).

GN TRPD2 OR SCO3212 OR SCE8\_05C.

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomyceinae; Streptomyctaceae; Streptomyces.

OX NCBI\_TaxID=1902;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3 (2) / M145;

RX MEDLINE=21996410; PubMed=12000953;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L., Thomson N.R., James K.D., Quail M.A., Kiser R., Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M., Cronin A., Fraser A., Goble A., Haddilo J., Hornsby T., Howarth S., Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., Rabbinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Seeger K., Saunders D., Sharp S., Squares R., Taylor K., Warren T., Wierzgorak A., Woodward J., Barrell B.G., Parkhill J., Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces coelicolor A3 (2)." ;

RL Nature 417:141-147 (2002).

CC -!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosyl-diphosphate = CC N-5'-Phosphoribosyl-anthraniilate + diphosphate.

CC -!- PATHWAY: Tryptophan biosynthesis; second step.

CC -!- SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase family.

CC

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CC

DR PIR; AL939115; T36304; T36304.

DR HAMAP; MF\_00211; -; 1.

DR InterPro; IPR005940; Ant phospho\_trans.

DR InterPro; IPR000312; Glyco\_trans\_N;-3.

DR Pfam; PF03885; Glycos\_transf\_N;-1.

DR Pfam; PF00591; Glycos\_transf\_F;-3; 1.

DR	TIGRFAMs; TIGR01525; ATPase-IB_hvy; 1.
DR	TIGRFAMs; TIGR01494; ATPase_P-type; 3.
DR	PROSITE; PS00154; ATPase_E1_E2; 1.
KW	Tryptophan biosynthesis; Transferase; Glycosyltransferase;
KW	Complete proteome;
SEQUENCE	335 AA; 34536 MW; 2706194E00B2F0D CRC64;
Query Match	Score 77; DB 1; Length 335;
Best Local Similarity	34.5%; Pred. No. 6.5;
Matches 30; Conservative	9; Mismatches 36; Indels 12; Gaps 4;
Qy	7 LGQLVALCSAAAFLVGSA---KPVAAQYAALESA---EAGAGTLANPLGTL-NP 56
Db	117 LGVRIDLGAEPAACIDRGTFLFAPVFFHD-AFRHTAGBRRELGARTVNLLGPLCNP 174
Qy	57 LKLULSSGLGPNNHLEGGQKRCVAELG 83
Db	175 SGARLPTLVGSRLVEPMTEVLERLG 201
RESULT 7	
ID	COPA_HELFE STANDARD; PRT; 732 AA.
AC	032619;
DT	15-JUL-1998 (Rel. 36, Created)
DT	15-JUL-1998 (Rel. 36, Last sequence update)
DT	15-MAR-2004 (Rel. 43, Last annotation update)
DE	Copper transporting ATPase (EC 3.6.3.4).
GN	COPA.
OS	Helicobacter felis.
OC	Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC	Helicobacterales; Helicobacter.
OX	NCBI_TaxID=214;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 49179.
RX	MEDLINE=98101471; PubMed=9440521;
RA	Bailey D., Waengler S., Weitzenecker T., Steinhilber W., Volz J.,
RA	Przybylski M., Schaefer K.P., Sachs G., Melchers K.,
RA	"Properties of the P-type ATPases encoded by the copA operons of Helicobacter pylori and Helicobacter felis.";
RT	J. Bacteriol. 180:317-329 (1998).
RU	J. Bacteriol. 180:317-329 (1998).
CC	-!- FUNCTION: PROBABLY INVOLVED IN COPPER EXPORT.
CC	-!- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+) (In) = ADP + phosphate + Cu (2+) (Out).
CC	-!- SUBCELLULAR LOCATION: Integral membrane protein.
CC	-!- SIMILARITY: Belongs to the cation transport ATPases family (P-type ATPases). Subfamily IB.
CC	-!- SIMILARITY: Contains 1 HMA domain.
CC	This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
CC	EMBL; AJ001932; CAA05104_1; -.
DR	PIR; T47259; TA7269.
DR	InterPro; IPR002469; ATPase-IB1_Cu.
DR	InterPro; IPR006403; ATPase-IB1_Fny.
DR	InterPro; IPR006416; ATPase-IB_Fny.
DR	InterPro; IPR001757; ATPase_E1-E2.
DR	InterPro; IPR001756; Cu_ATPase.
DR	InterPro; IPR00250; E1-E2_ATPase_Reg.
DR	InterPro; IPR005121; Heavy_Me_transp.
DR	InterPro; IPR005834; Hydrolase.
DR	InterPro; IPR006191; Metal_bind.
DR	Pfam; PF00122; E1-E2_ATPase; 1.
DR	Pfam; PF00403; FMA: 1.
DR	Pfam; PF00702; Hydrolase; 1.
DR	PRINTS; PRO0119; CUAATPASE.
DR	PRINTS; PRO0943; CUATPASE.
DR	TIGRFAMs; TIGR01511; ATPase-IB1_Cu; 1.
DR	TIGRFAMs; TIGR01494; ATPase_P-type; 3.
DR	PROSITE; PS00154; ATPase_E1_E2; 1.
KW	Transport; Ion transport; Copper transport; Hydrolase; ATP-binding; Metal-binding; Copper; Magnesium; Phosphorylation; CYTOPLASMIC (POTENTIAL).
FT	DOMAIN 1 88
FT	TRANSMEM 89 109
FT	DOMAIN 110 122
FT	TRANSMEM 142 142
FT	DOMAIN 143 149
FT	TRANSMEM 150 170
FT	DOMAIN 171 187
FT	TRANSMEM 188 208
FT	DOMAIN 209 336
FT	TRANSMEM 337 359
FT	DOMAIN 360 365
FT	TRANSMEM 366 383
FT	DOMAIN 384 663
FT	TRANSMEM 664 683
FT	DOMAIN 684 694
FT	TRANSMEM 695 713
FT	DOMAIN 714 732
FT	MOD_RES 3 69
FT	METAL 421 421
FT	METAL 13 13
FT	METAL 16 16
FT	METAL 609 609
FT	METAL 613 613
SQ	SEQUENCE 732 AA; 78653 MW; 7105107EA949ERD CRC64;
Query	Match 15.1%; Score 76; DB 1; Length 732;
Best Local Similarity	26.3%; Pred. No. 16; Mismatches 39; Indels 42; Gaps 6;
Matches 35; Conservative 17; Standard:	
Qy	6 LIGCIVALSCTSSAAFLVGSAKPVAAL---ESAAEAGAG-----
Db	447 LILTCASLEAQSERVIAGIVAHKEQGIALQEYQAKPGFGIKGVGDQIKAQNLE 506
Qy	46 --TIANPLIGTLPNLKLSS---LGIPV--NHLIEGSQKCYAELGPQAVGA-----
Db	507 FFNPNPFPCTLEGQVFVGETQLGVVVLADSLKEGSKEAISEL-KALGVKTTLSSGD 564
Qy	90 ---VKALKLNG 98
Db	565 NLENVRALATQLG 577
RESULT 8	
MDCL_HUMAN	STANDARD; PRT; 362 AA.
ID	O91HK6; 447 LILTCASLEAQSERVIAGIVAHKEQGIALQEYQAKPGFGIKGVGDQIKAQNLE 506
AC	47 LILTCASLEAQSERVIAGIVAHKEQGIALQEYQAKPGFGIKGVGDQIKAQNLE 506
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Mesoderm development candidate 1.
GN	Homo sapiens (Human)
RC	SEQUENCE FROM N.A.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
NCBI_TaxID	9606;
OX	
RN	
RP	
RC	TISSUE=Retina;
RC	Medline=21145589; PubMed=11247670;
RC	Lee L., Kartar M.S., Zhang L., DeRossi C., Shi Y., Perkins S., Feldman M., McCombie W.R., Holdener B.C.; "Identification of mesoderm development (mesod) candidate genes by comparative mapping and genome sequence analysis"; RIL Genomics 72:88-98 (2001).
RT	-!- SIMILARITY: SOME, TO TALIN.
CC	
CC	

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Query	Match	14.9%	Score	75;	DB	1;	Length	362;
	Best Local Similarity	35.4%	Pred.	No.	11;			
	Matches	28;	Conservative	Mismatches	33;	Indels	12;	Gaps
Qy	3	LAALIIGCVALS	-CSAAAFLYGSAKA	KPVAQP	-----	VAALESAAEAGAGT	L-ANP	50
Db	112	LVELGDIIVSILTECSAHAAYLAAAVATFGAQPAQPGILDYRYVTRCRIVEQQCAVLRA	T	P	-----	-----	-----	171
Qy	51	LGTLNPFLKLSSLGIPVN	69					
Db	172	LGTLNPFLKLSSLGIPVN	69					
Qy	172	LGTLNPFLKLSSLGIPVN	69					

RESULT 9						
C1 MOUSE		STANDARD;	PRT;	362 AA.		
Q9ER8	MDCL MOUSE				ID SN1_MOUSE	STANDARD;
28-FEB-2003	(Rel. 41, Created)				ID Q60570;	PRT; 779 AA.
28-FEB-2003	(Rel. 41, Last sequence update)				AC DT 01-NOV-1997	(Rel. 35, Created)
10-OCT-2003	(Rel. 42, Last annotation update)				DT 16-OCT-2001	(Rel. 40, Last sequence update)
MESDC1	Mesoderm development candidate 1.				DT 15-MAR-2004	(Rel. 43, Last annotation update)
Mus musculus (Mouse)	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				DB Probable serine/threonine protein kinase SNFLIK (EC 2.7.1.-) (HRT-20)	(Myocardial SNF1-like kinase).
NCBI_TaxID=10090;					DB SNFLIK OR MSK	
					OS Mus musculus (Mouse)	
					OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
					OC NCBII_TaxID=10090;	
[1]					RN [1]	
					RP	
					SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.	
					RC TISSUE=Embryo;	
					RA Rui J.C.	
					RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.	
					RN [2]	

	SEQUENCE OF 1-415 FROM N.A., AND TISSUE SPECIFICITY.
[2]	SEQUENCE FROM N.A. MEDLINES=22388257; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schaefer C.P., Blat N.K., Aitken S.F., Zesberg B., Buetow K.H., Schaefer C.P., Blat N.K., Hopkins R.K., Jordan H., Moore T., Wang M.S.I., Wong L., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Udin T.B., Toshiyuki S., Carninci P., Prange C., Raba S.S., Logueillo N.A., Peters G.J., Abramson R.D., Mullally S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richardson S., Worley K.C., Hale S., Garcia A.M., Hulyk S.W., Villarich D.K., Muzyz D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Heilcon E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whalesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Salska U., Smailus D.E., Schnierch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.", Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
L	- - TISSUE SPECIFICITY: Ubiquitous.
C	- - SIMILARITY: SOME, TO TALIN.
R	RP TISSUE-EMBRYO;
RX	RP MEDLINE=95200798; PubMed=7893599;
RC	RP Ruiz J.C.; Conlon F.L.; Robertson E.J.;
PA	RP Identification of novel protein kinases expressed in the myocardium of the developing mouse heart., Mech. Dev. 48:153-164 (1994).
RT	RT TISSUE SPECIFICITY: Expressed in lung, skin, ovary, heart and stomach. No expression in brain, liver or skeletal muscle.
RT	RT SIMILARITY: Belongs to the Ser/Thr Family of Protein Kinases. SNF1 subfamily.
RL	RL - - TISSUE SPECIFICITY: Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce">http://www.isb-sib.ch/announce</a> or send an email to license@isb-sib.ch).
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CC	CC EMBL; P24941; 1AQI; MGDB; MGDB:104154; Snf1k.
DR	DR InterPro; IPR000719; Prot kinase.
DR	DR InterPro; IPR008271; Ser_Chr_pk1n_AS.
DR	DR InterPro; IPR002230; Ser-thr_pk1n-AS.

DR InterPro; IPR001245; TYR\_Dkinase.  
 DR InterPro; IPR000449; UBA\_domain.  
 DR PRINTS; PRO0109; TYRKINASE.  
 DR ProDom; PF00069; Dkinase\_1.  
 DR SMART; SM00220; S\_TMC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS00011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR PROSITE; PS50030; UBA; 1.  
 KW transerase; Serine/threonine-protein kinase; ATP-binding.  
 FT DOMAIN 27 278 PROTEIN KINASE.  
 FT DOMAIN 303 343 UBA.  
 NP BIND 33 41 ATP (BY SIMILARITY).  
 FT BINDING 56 56 ATP (BY SIMILARITY).  
 FT ACT SITE 149 149 BY SIMILARITY.  
 SQ SEQUENCE 779 AA; 85027 MW; 7B08131BCA6D9C4E CRC64;

Query Match 14.7%; Score 74; DB 1; Length 779;  
 Best Local Similarity 32.9%; Pred. No. 26;  
 Matches 26; Conservative 11; Mismatches 30; Indels 12; Gaps 3;

Qy 10 CVALSCSSAAAPLVGSAKPVQAQPVALESAABAGATLNP-LGTINPKULLSSIGIP 67  
 Db 490 CIVSSSATASSESEGTSDDSLCPFSASEGPAGLGS-LATPGLLGSSPPVRLASPEL-- 545

Qy 6 VNHLLRGSSQKCVQAEGLPQO 86  
 Db 546 -----GSQSATPVLQTQ 558

RESULT 11  
 DKS WIGBR STANDARD: PRT; 626 AA.  
 ID Q8D357; AC Q9R081; DT 16-OCT-2003 (Rel. 42, Created)  
 DT 10-OCT-2003 (Rel. 42, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE 1-deoxy-D-xylulose-5-phosphate synthase (EC 2.2.1.7) (1-  
 deoxyxylulose-5-phosphate synthase) (DXPS) (DXPS).  
 GN WIGBR1440  
 OS Wigglesworthia glossinidria brevipalpis.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Wigglesworthia.  
 OX NCBI\_TaxID=36870;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22297710; PubMed=12219091;  
 RA Akman L.; Yamashita A.; Watanabe H.; Oshima K.; Shiba T.; Hattori M.;  
 RA Aksoy S.; RT "Genome sequence of the endocellular obligate symbiont of tsetse  
 flies, Wigglesworthia glossinidria.";  
 RT Nat. Genet. 32:402-407(2002).  
 CC 1-PUNCTION: Catalyzes the acyloin condensation reaction between C  
 atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield  
 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).  
 CC -!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-  
 deoxy-D-xylulose 5-phosphate + CO<sub>2</sub>.  
 CC -!- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By  
 similarity).  
 CC -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; first step.  
 CC -!- PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first  
 step.  
 CC -!- SIMILARITY: Homodimer (By similarity).  
 CC -!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.

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RESULT 12  
 SNIL\_RAT STANDARD: PRT; 776 AA.  
 ID SNIL\_RAT AC Q9R081; DT 16-OCT-2001 (Rel. 40, Created)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Probable serine/threonine protein kinase SNFLIK (EC 2.7.1.-) (Salt-  
 inducible protein kinase) (protein kinase KD2).  
 GN SNFLIK OR SIK OR KID2.  
 OS Rattus norvegicus (Rat).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX STRAIN-Sprague-Dawley; TISSUE=Adrenal gland;  
 RX MEDLINE=993018; PubMed=1040390;  
 RA Wan Z.; Takemori H.; Haider S.K.; Nonaka Y.; Okamoto M.;  
 RA Herschman H.R.; RT "Cloning of a novel kinase (SK) of the SNFL1/AMPK family from high  
 salt diet-treated rat adrenal.";  
 RL FEBs Lett. 453:135-139 (1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=993018; PubMed=1040390;  
 RA Feldman J.D.; Vician L.; Crispino M.; Hoe W.; Baudry M.;  
 RA Wang Z.; Takemori H.; Haider S.K.; Nonaka Y.; Okamoto M.;  
 RA Herschman H.R.; RT "The Kidd gene encodes a protein kinase induced by depolarization in  
 brain.";  
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.  
 CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNFL1  
 CC subfamily.  
 CC -!- SIMILARITY: Contains 1 UBA domain.

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DR EMBL; AB024480; BAA82673.1;  
 DR AF106937; AAF14191.1;  
 DR EMBL; AB024480; BAA82673.1;  
 DR AF106937; AAF14191.1;

DR	HSSP; P24941; 1AQ1.	DR	InterPro; IPR000719; Prot_kinase.	DR	InterPro; IPR000719; tRNA_synt_AlA.		
DR	InterPro; IPR008271; Ser_Thr_Pkinase.	DR	Pfam; PF02272; DHEA1; 1.	DR	Pfam; PF01411; tRNA-synt_2c; 1.		
DR	InterPro; IPR002290; Ser_Thr_Pkinase.	DR	PRINTS; PR0930; TRNASTHALLA.	DR	PRINTS; PR0930; TRNASTHALLA.		
DR	InterPro; IPR000449; UBA_domain.	DR	TIGRFAMS; TIGR00344; alias; 1.	DR	TIGRFAMS; TIGR00344; alias; 1.		
DR	Pfam; PF00069; Pkinase; 1.	DR	PROSITE; PS50060; AA_tRNA_LIGASE_I.I_ALA; 1.	DR	PROSITE; PS50060; AA_tRNA_LIGASE_I.I_ALA; 1.		
DR	ProDom; P000001; Prot_kinase; 1.	KW	Aminocyl-tRNA synthetase; Protein Biosynthesis; Ligase; ATP-binding.	KW	Aminocyl-tRNA synthetase; Protein Biosynthesis; Ligase; ATP-binding.		
DR	SMART; SM0220; S_TKc; 1.	SQ	SEQUENCE BB2 AA; 97454 MW;	SQ	SEQUENCE BB2 AA; 97454 MW;		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	Query Match	14.6%; Score 73.5%; DB 1; Length 802;	Query Match	14.6%; Score 73.5%; DB 1; Length 802;		
DR	PROSITE; PS00011; PROTEIN_KINASE_DON; 1.	Best Local Similarity 32.6%; Pred. No. 32;	Best Local Similarity 32.6%; Pred. No. 32;	Best Local Similarity 32.6%; Pred. No. 32;	Best Local Similarity 32.6%; Pred. No. 32;		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	Mismatches 30; Conservative 12; Mi matches 3;	Mismatches 30; Conservative 12; Mi matches 3;	Mismatches 30; Conservative 12; Mi matches 3;	Mismatches 30; Conservative 12; Mi matches 3;		
DR	PROSITE; PS00030; UBA; 1.	Indels 3; Gaps 2;	Indels 3; Gaps 2;	Indels 3; Gaps 2;	Indels 3; Gaps 2;		
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.	Qy	6 LIGGLVALCSAAAFLVGSAPKAQPVAALESAMAEAGCTLANGLTNPKLKLISSLG 65	Qy	6 LIGGLVALCSAAAFLVGSAPKAQPVAALESAMAEAGCTLANGLTNPKLKLISSLG 65		
FT	DOMAIN 27 PROTEIN_KINASE.	Db	681 LCGGCHVRRTGEIGFLIRSEEAVAGVRIE-AVTGEGPAIRFARGSLNRLKALERLIE 738	Db	681 LCGGCHVRRTGEIGFLIRSEEAVAGVRIE-AVTGEGPAIRFARGSLNRLKALERLIE 738		
FT	DOMAIN 303 343 UBA.	FT	ATP (BY SIMILARITY).	FT	ATP (BY SIMILARITY).		
FT	NP_BIND 33 41 ATP (BY SIMILARITY).	FT	ATP (BY SIMILARITY).	FT	ATP (BY SIMILARITY).		
FT	BINDING 56 56 BY SIMILARITY.	FT	ACT SITE 149 149 BY SIMILARITY.	FT	ACT SITE 149 149 BY SIMILARITY.		
FT	CONFFLICT 473 473 R->K (IN REF. 2).	FT	CONFFLICT 473 473 R->K (IN REF. 2).	FT	CONFFLICT 473 473 R->K (IN REF. 2).		
SQ	SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17B6E CRC64;	Qy	66 IPVNLHJEGSKQKVAAELGPQAVGATKALKL 97	Qy	66 IPVNLHJEGSKQKVAAELGPQAVGATKALKL 97		
RESULT 14	Query Match 14.6%; Score 73.5%; DB 1; Length 776;	Db	739 VGEAALERLEKLKLLAEI-KEKEREVESLKLRL 769	Db	739 VGEAALERLEKLKLLAEI-KEKEREVESLKLRL 769		
SYA - THETH	STANDARD; PRT; 882 AA.	SYU - THETH	STANDARD; PRT; 397 AA.	SYU - THETH	STANDARD; PRT; 397 AA.		
AC	P74494; 01-NOV-1997 (Rel. 35, Created)	AC	Q8UC45; 28-FEB-2003 (Rel. 41, Created)	AC	Q8UC45; 28-FEB-2003 (Rel. 41, Last sequence update)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)	DT	01-NOV-1997 (Rel. 41, Last sequence update)	DT	10-OCT-2003 (Rel. 42, Last annotation update)		
DB	490 CIVSSAAVSSSEGTSDDSCDPSFASSEGPAQIGGG-LATPGLGSSPVLASPPFL--	DB	545 Suciny1-coA synthetase beta chain (EC 6.2.1.5) (SCS-beta).	DB	545 Suciny1-coA synthetase beta chain (EC 6.2.1.5) (SCS-beta).		
Qy	10 CYVALCSAAAFLVGSAAPKAQPVAALESAAABAGTTLANP--LGTPLNPKLKLSSLGIP 67	GN	GN ATU2638 OR AGR C 4780.	GN	GN ATU2638 OR AGR C 4780.		
Db	490 CIVSSAAVSSSEGTSDDSCDPSFASSEGPAQIGGG-LATPGLGSSPVLASPPFL--	OS	Agrobacterium tumefaciens (strain C58 / ATCC 333970).	OS	Agrobacterium tumefaciens (strain C58 / ATCC 333970).		
Qy	68 VNHLIEGSSQKCYAELGPQA-VGA 89	OC	Bacteria; Proteobacteria; Alpha proteobacteria; Rhizobiales;	OC	Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.		
Db	546 ----S9QSATPVLQSSAGLGA 562	OX	NCBI_TAXID=176299;	OX	NCBI_TAXID=176299;		
RN [1]	SEQUENCE FROM N.A.	RN [1]	SEQUENCE FROM N.A.	RN [1]	SEQUENCE FROM N.A.		
RN	MEDLINE=21608550; PubMed=11743193;	RX	MEDLINE=21608550; PubMed=11743193;	RX	MEDLINE=21608550; PubMed=11743193;		
RX	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Almeida N.F.Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D.Sr., Chapman P., Clendenning J., Deathrage G., Gillet W., Kuyavim T., Levy E., Li M.-J., McClelland E., Palmeri A., Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W., "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.", Science 294:2323-2328(2001).	RX	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Almeida N.F.Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D.Sr., Chapman P., Clendenning J., Deathrage G., Gillet W., Kuyavim T., Levy E., Li M.-J., McClelland E., Palmeri A., Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W., "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.", Science 294:2323-2328(2001).	RX	Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P., Okura V.K., Zhou Y., Chen L., Almeida N.F.Jr., Woo L., Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D.Sr., Chapman P., Clendenning J., Deathrage G., Gillet W., Kuyavim T., Levy E., Li M.-J., McClelland E., Palmeri A., Raymond C., Rouse G., Saenphimachak C., Wu Z., Romero P., Gordon D., Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M., Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M., Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V., Nester E.W., "The genome of the natural genetic engineer Agrobacterium tumefaciens C58.", Science 294:2323-2328(2001).		
RN [2]	SEQUENCE FROM N.A.	RN [2]	SEQUENCE FROM N.A.	RN [2]	SEQUENCE FROM N.A.		
RX	MEDLINE=21608551; PubMed=11743194;	RX	MEDLINE=21608551; PubMed=11743194;	RX	MEDLINE=21608551; PubMed=11743194;		
RA	Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L., Quirollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Holmier K., Gordon J., Vaudin M., Tartchouk O., Epp A., Lappes C., Markelz B., Flanagan C., Allinger N., Doughty D., Scott C., Lomo C., See C., Strub G., Clelo C., Slater S.;	RA	Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L., Quirollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Holmier K., Gordon J., Vaudin M., Tartchouk O., Epp A., Lappes C., Markelz B., Flanagan C., Crowell C., Gursen J., Lomo C., See C., Strub G., Clelo C., Slater S.;	RA	Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L., Quirollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Holmier K., Gordon J., Vaudin M., Tartchouk O., Epp A., Lappes C., Markelz B., Flanagan C., Crowell C., Gursen J., Lomo C., See C., Strub G., Clelo C., Slater S.;	RA	Goddner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L., Quirollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L., Holmier K., Gordon J., Vaudin M., Tartchouk O., Epp A., Lappes C., Markelz B., Flanagan C., Crowell C., Gursen J., Lomo C., See C., Strub G., Clelo C., Slater S.;
RA	"A biologically active 53 kDa fragment of overproduced alanyl-tRNA synthetase from <i>Thermus thermophilus</i> HB8 specifically interacts with tRNA ala acceptor helix."	RA	"A biologically active 53 kDa fragment of overproduced alanyl-tRNA synthetase from <i>Thermus thermophilus</i> HB8 specifically interacts with tRNA ala acceptor helix."	RA	"A biologically active 53 kDa fragment of overproduced alanyl-tRNA synthetase from <i>Thermus thermophilus</i> HB8 specifically interacts with tRNA ala acceptor helix."		
RA	Nucleic Acids Res. 25:2737-2744 (1997)	RA	Nucleic Acids Res. 25:2737-2744 (1997)	RA	Nucleic Acids Res. 25:2737-2744 (1997)		
CC	- - CATALYTIC ACTIVITY: AMP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala).	CC	- - CATALYTIC ACTIVITY: AMP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala).	CC	- - CATALYTIC ACTIVITY: AMP + L-alanine + tRNA(Ala) = AMP + diphosphate + L-alanyl-tRNA(Ala).		
CC	- - SUBCELLULAR LOCATION: Cytoplasmic.	CC	- - SUBCELLULAR LOCATION: Cytoplasmic.	CC	- - SUBCELLULAR LOCATION: Cytoplasmic.		
CC	- - SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.	CC	- - SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.	CC	- - SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.		
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CC	DR	DR	DR	DR	DR		
CC	HAMP; MF_00016; -; 1.	CC	Y03363; CAA69650.1; -.	CC	Y03363; CAA69650.1; -.		
CC	InterPro; IPR003156; DHH1.	CC	InterPro; IPR003156; DHH1.	CC	InterPro; IPR003156; DHH1.		
CC	InterPro; IPR002318; tRNA-synt_2c.	CC	InterPro; IPR002318; tRNA-synt_2c.	CC	InterPro; IPR002318; tRNA-synt_2c.		

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EMBL; AE009211; AAL43619\_1;

DR PIR; AE2900; AE2900.

DR PIR; F97675; F97675.

DR HAMAP; MF\_00558; -1.

DR InterPro; IPR003135; ATP\_grasp.

DR InterPro; IPR005809; CoA\_lig\_beta.

DR Pfam; PF02222; ATP\_grasp; 1.

DR Pfam; PF0549; Ligase-Cox; 1.

DR TIGRFAMS; TIGR01016; succoCoA\_beta; 1.

DR PROSITE; PS01217; SUCCINYL\_COA\_LIG\_3; FALSE\_NEG.

KW Ligase; tricarboxylic\_acid\_cycle; Complete\_proteome.

SEQUENCE 397 AA; 41899 MW;

222C1A325763FF CRC64;

CC or send an email to license@isb-sib.ch).

CC ---

CC EMBL; X32591; CAA53335\_1;

CC EMBL; X71942; CAA5744\_1;

CC PIR; D47746; D47746.

CC HSSP; Q63245;

CC TRANSFAC; T02442; -.

CC MGI; MGI\_1347468; Foxbx2.

CC InterPro; IPR001756; TE\_Fork\_head.

CC Pfam; PR00250; Fork\_head; 1.

CC PRINTS; PR00053; FORKHAD.

CC PRODOM; PD000425; TP\_Fork\_head; 1.

CC SMART; SM00339; FH\_1;

CC PROSITE; PS00657; FORK\_HEAD\_1;

CC PROSITE; PS00658; FORK\_HEAD\_2;

CC PROSITE; PS50039; FORK\_HEAD\_3;

CC DNA binding; Nuclear\_protein; Transcription\_regulation.

CC ---

CC KW FORK HEAD.

CC FT DOMAIN 12 103

CC FT DOMAIN 139 153

CC FT DOMAIN 156 162

CC FT DOMAIN 163 172

CC FT DOMAIN 217 231

CC FT DOMAIN 249 258

CC FT DOMAIN 321 330

CC FT DOMAIN 396 399

CC SEQNE 428 AA; 45170 MW;

CC DB8A8EFD1E94AB10 CRC64;

Query Match 14.1%; Score 71; DB 1; Length 428;  
Best Local Similarity 29.2%; Pred. No. 28;  
Matches 33; Conservative 17; Mismatches 43; Indels 20; Gaps 6;  
Qy 11 VALSSSSAAAFLVGSAKPVQAQ-PVVALESRAEGGTIANPLGTINPL-----KL 59  
Db 220 VAAARAAAIAAVGSVGRISQFPYVGLSIAAAAASSTGFKHPFALENLIGRDYKG 279

Query Match 14.1%; Score 71; DB 1; Length 428;  
Best Local Similarity 29.2%; Pred. No. 28;  
Matches 33; Conservative 17; Mismatches 43; Indels 20; Gaps 6;

Qy 60 LLSSGIP----VNHL---TEGS-QKCVAAELGPQPGVAKALKALGALTFG 104  
Db 280 VLQAGCLPLASVMHLLGYPVGQLSNVVGSVWPH-VGMDSVAAAAAAAAG 331

Search completed: June 2, 2004, 20:19:36  
Job time : 5.04538 secs

RESULT 15  
FXB2\_MOUSE  
ID FXB2\_MOUSE  
AC Q64733;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Forthead box protein B2 (Transcription factor FXH-4).  
GN FOXB2 OR FXH4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata;Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
RN [1] STRAIN\_N=129; PubMed=8861101;  
RN MEDLINE=97014266;  
RN Kaestner K.H., Schuetz G., Monaghan A.P.;  
RN "Expression of the winged helix genes *fxh-4* and *fxh-5* defines domains  
RT in the central nervous system.",  
RL Mech. Dev. 55:221-230 (1996).  
RN [2] SEQUENCE FROM N.A.  
RN STRAIN\_N=129;  
RN MEDLINE=93361500; PubMed=7689224;  
RN Kaestner K.H., Lee K.H., Schliendorff J., Hiemisch H.,  
RN Monaghan A.P., Schuetz G.;  
RN "Six members of the mouse *forkhead* gene family are developmentally  
RT regulated.",  
RL Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631 (1993).  
RN ---  
RN -1- SUBCELLULAR LOCATION: Nuclear.  
RN -1- DEVELOPMENTAL\_STAGE: Expressed during embryogenesis.  
RN -1- SIMILARITY: Contains 1 fork-head domain.

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GenCore version 5.1.6  
(c) 1993 - 2004 Compugen Ltd.

Copyright - protein search, using sw model

Run on: June 2, 2004, 20:14:10 ; Search time 7.07942 Seconds  
(without alignments)  
1413.099 Million cell updates/sec

Title: US-09-700-770-9  
Perfect score: 502  
Sequence: 1 MKIAALIGLVALSCSSAAA.....QAVGAVKALKALLGALTVEFG 104

Scoring table: BL05UM62  
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR78:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	81	16.1	496	2 T0931	probable phosphodiesterase I
2	79.5	15.8	1381	2 S60004	hypothetical prote
3	77.5	15.4	601	2 T35054	probable transport
4	77	15.3	335	2 T36304	probable anthranil
5	76	15.1	355	2 AD2973	hypothetical prote
6	76	15.1	355	2 G98309	probable ABC trans
7	76	15.1	699	2 HB7275	thio-disulfide int
8	76	15.1	732	2 T47269	copper-transportin
9	75	15.0	544	2 H77647	hypothetical prote
10	73.5	14.6	331	2 CB4358	transport protein
11	73	14.5	502	2 FB8553	probable aldehyde
12	73	14.5	584	2 BB87315	gamma-glutamyltran
13	73	14.5	1279	2 T13613	hypothetical prote
14	72	14.3	236	2 A556010	amastigote-specific
15	72	14.3	397	2 AE2900	buccinyl-CoA synth
16	72	14.3	397	2 F97675	buccinyl-CoA synth
17	72	14.3	528	2 D70968	hypothetical prote
18	71.5	14.2	462	2 BB87334	L-Serine dehydratase
19	71.5	14.2	874	2 AC3070	ATP-dependent Clp
20	71.5	14.2	887	2 F98216	endopeptidase clp
21	71	14.1	440	2 CB3368	probable MFS trans
22	70.5	14.0	668	2 G85160	heat shock protein
23	70.5	14.0	831	2 D71409	probable endopepti
24	70	13.9	431	2 C85178	hypothetical prote
25	70	13.9	452	2 T46147	zinc finger protei
26	70	13.9	477	2 D82179	probable multidrug
27	69.5	13.8	244	2 S75653	hypothetical prote
28	69.5	13.8	396	2 G7554	probable prote
29	69.5	13.8	423	2 CT0582	probable PPE prote

#### ALIGNMENTS

RESULT 1	T0931	probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9)
C;Species:	Arabidopsis thaliana (mouse-ear cress)	
C;Date:	16-Jul-1999 #sequence_change 16-Aug-2002	
C;Accession:	T0931	
R;Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mayer, K		
A;Submitted to the Protein Sequence Database, June 1999		
A;Reference number: Z16897		
A;Accession: T0931		
A;Molecule type: DNA		
A;Cross-references: EMBL: AL073344; GSPDB: GN00062; ATSP: T1614.190		
A;Experimental source: cultivar Columbia; BAC clone T16L4		
C;Genetics:		
A;Gene: ATSP:T16L4.190		
A;Map Position: 4		
C;Superfamily: human phosphodiesterase I		
C;Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase		
Query Match Score 81; DB 2; Length 496;		
Best Local Similarity 41.3%; Pred. No. 5.2;		
Matches 26; Conservative 14; Mismatches 17; Indels 6; Gaps 3;		
Qy 6 LIGGLVALCSAAAFVGSKAPVVALESAAPAGA--GTLANPLGLIN-PDKLILS 62		
Db 57 LIVTCIALSASAFAFLFFSSQ--KPVLNSUNIQSKSPAFDRSVARPLKCLDKPVVLLIS 113		
Qy 63 SIG 65		
Db 114 SDG 116		

Query Match 1	Score 79.5; Pred. No. 20;	DB 2; Length 1381;	Db 117 LGVRIDLGAEEAACLDRGTITELLAPVFRP--AFRHTAGPRRELGARTVNLLGPLCNP 174
Best Local Similarity 27.08%; Matches 25;	Conservative 15; Mismatches 23;	Indels 27; Gaps 3;	Qy 57 LKLLLOSSLGGPVNHLEGGSKQCVNLG 83
Qy 1.1 VALSCSAAFLVGSAKPAQVALESAAEAGT-----LANPLG-----52			Db 175 SGARLRLGVSRELVEPMTEEVLRG 201
Db 27 IAMPCSTNSFFERGTPEPHESIGTSSESIGMGTTHRSPRLNDDEVINGKGHESDPVH 86			
RESULT 5			
AD2973 hypothetical protein Atu3389 [Imported] - Agrobacterium tumefaciens (strain C58, D4P)			
C;Species: Agrobacterium tumefaciens			
C;Date: 11-Jan-2002 #text_change 18-Nov-2002			
C;Accession: AD2973			
R;Wood, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Wohler, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayvin, T.; Levy, R.; Li, M.; McCaffery, P.; Romero, P.; Zhang, S.			
T35054 transport system permease protein - Streptomyces coelicolor			
C;Species: Streptomyces coelicolor			
C;Accession: T35054			
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.			
A;Reference number: Z21566			
A;Accession: T35054			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-601 <SEE>			
A;Cross-references: ENB:AU031371; PIDN:CRX20556.1; GSPDB:GN00070; SCOEDB:SC4G2.19			
A;Experimental source: strain A3 (2)			
C;Genetics:			
A;Gene: SCOEDB:SC4G2.19			
Qy 53 -----TIANPLKLSSGIPYNHLIEGSQ 76			
Db 87 VYRAPRTHPRRL--ELPIGVNNLGESQ 113			
RESULT 3			
T35054 probable transport system permease protein - Streptomyces coelicolor			
C;Species: Streptomyces coelicolor			
C;Accession: T35054			
R;Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.			
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A;Experimental source: strain A3 (2)			
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Qy 54 Query Match 15.4%; Score 77.5; Pred. No. 13; DB 2; Length 601;			
Best Local Similarity 30.7%; Matches 42; Conservative 10; Mismatches 48; Indels 37; Gaps 4;			
Db 426 LVALLYTAVAGSGAATPLAVGAYAWPLAHTSSLRQERATHITATKGLGAGPVHLL 485			
Qy 46 -----TIANPLGTINPLKLSSGIPYNHLIEGSQ 85			
Db 486 RHEILPPAVPPVPLRHALLRPLGVALLASLIGFLGQAQPSPENGLLIAENQPYAERAPW 545			
Qy 47 AVGAVKAKALKALLGATV 102			
Db 546 AVLAPAVLALLGALAV 562			
RESULT 6			
G98309 probable ABC transporter permease protein MJ0087 AGR_L_2865 [Imported] - Agrobacteri			
C;Species: Agrobacterium tumefaciens			
C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002			
C;Accession: G98309			
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Quroollo, B.; Golz, A.; Liu, F.; Wollam, C.; Blanchard, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, A.; Rill, F.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, A.; Science 294, 2323-2328, 2001.			
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium			
A;Reference number: A97359; PMID:21608551; PMID:11743194			
A;Accession: G98309			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-355 <KUR>			
A;Cross-references: GB:AE008689; PIDN:AAU44202.1; PID:917741781; GSPDB:GN00187			
C;Genetics:			
A;Gene: Atu3389			
A;Map position: linear chromosome			
Qy 55 Query Match 15.1%; Score 76; Pred. No. 11; DB 2; Length 355;			
Best Local Similarity 23.3%; Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;			
Db 55 KLAALLGHCVVALCSSSAAAFLVGSAKEVAQPVAALESAAEAGGTIANPLGTINPLKLL 61			
Qy 56 24 RILLVLGFLFLCFSMADMALGPARYTLSEVLA-----TIADPAAVGNQLRVVI 73			
Qy 57 62 SSLGIPVNH-----IEGSQKCV-----ELGPQAVGAVYAKALLGATVTF 103			
Db 58 74 WDIRMPITALMAYTVGASHSVAGMQTILSNPLASPFITLGTISAAASFGAALLLVGVIAF 133			
RESULT 7			
T36304 probable arabinanilate phosphoribotransferase - streptomyces coelicolor			
C;Species: Streptomyces coelicolor			
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Jan-2000			
C;Accession: T36304			
R;Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.			
A;Reference number: Z21604			
A;Accession: T36304			
A;Status: preliminary			
A;Gene: trpD; SCOEDB:SCB8.05c			
C;Superfamily: anthranilate phosphoribosyltransferase; trpD homology			
A;Molecule type: DNA			
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A;Experimental source: strain A3 (2)			
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A;Cross-references: EMBL:AL035654; PIDN:CAB38583.1; GSPDB:GN00070; SCOEDB:SCB8.05c			
A;Experimental source: strain A3 (2)			
C;Genetics:			
A;Gene: trpD; SCOEDB:SCB8.05c			
C;Superfamily: anthranilate phosphoribosyltransferase			
A;Molecule type: DNA			
A;Residues: 1-335 <SAU>			
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A;Experimental source: strain A3 (2)			
C;Genetics:			
A;Gene: trpD; SCOEDB:SCB8.05c			
C;Superfamily: anthranilate phosphoribosyltransferase			
A;Molecule type: DNA			
A;Residues: 1-335 <SAU>			
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A;Experimental source: strain A3 (2)			
C;Genetics:			
A;Gene: trpD; SCOEDB:SCB8.05c			
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A;Molecule type: DNA			
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A;Experimental source: strain A3 (2)			
C;Genetics:			
A;Gene: trpD; SCOEDB:SCB8.05c			
C;Superfamily: anthranilate phosphoribosyltransferase			
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A;Experimental source: strain A3 (2)			
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A;Gene: trpD; SCOEDB:SCB8.05c			
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A;Experimental source: strain A3 (2)			
C;Genetics:			
A;Gene: trpD; SCOEDB:SCB8.05c			
C;Superfamily: anthranilate phosphoribosyltransferase			
A;Molecule type: DNA			
A;Residues: 1-335 <SAU>			
A;Cross-references: EMBL:AL035654; PIDN:CAB38583.1; GSPDB:GN00070; SCOEDB:SCB8.05c			
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C;Genetics:			
A;Gene: trpD; SCOEDB:SCB8.05c			
C;Superfamily: anthranilate phosphoribosyltransferase			
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A;Residues: 1-335 <SAU>			
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Db	74 WDIRMPALMAVTGASLISVAGAQNYQITLSNPLASPTFISAAASFGAALALYGGVAF	133	Db	507 FENLNPNPGFTLEGICQVFVGTFETQILGVVVVLADSLXEGSKEAISEL - KALGVKTTLLSGD	564
Qy	90 ---VKALKALIG 98		Qy	90 ---VKALKALIG 98	
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C;Species: Caulobacter crescentus	C;Species: Caulobacter crescentus		C;Species: Aeropyrum pernix (strain K1)	C;Species: Aeropyrum pernix	
C;Accession: R87275	C;Accession: R87275		C;Date: 20-Aug-1999 #text_change 20-Aug-1999	C;Date: 20-Aug-1999 #text_change 20-Aug-1999	
R.;Laub, M.T.; Delboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hft, D.H.; Kolonin, J.; Emelava, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001	R.;Laub, M.T.; Delboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hft, D.H.; Kolonin, J.; Emelava, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.; Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001		R.;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999	R.;Kawarabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Tawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudo, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999	
A;Title: Complete Genome Sequence of Caulobacter crescentus.	A;Title: Complete Genome Sequence of Caulobacter crescentus.		A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerococcus viridans.	A;Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aerococcus viridans.	
A;Reference number: A87249; PMID:21173698;	A;Reference number: A87249; PMID:21173698;		A;Reference number: A72450; PMID:99310339;	A;Reference number: A72450; PMID:99310339;	
A;Accession: H87275	A;Accession: H87275		A;Accession: H72647	A;Accession: H72647	
A;Status: Preliminary	A;Status: Preliminary		A;Molecule type: DNA	A;Molecule type: DNA	
A;Residues: 1-699 <STO>	A;Residues: 1-699 <STO>		A;Cross-references: GB:AE005673; NID:913421344; PIDN:AAK22204.1; GSPDB:GN00148	A;Cross-references: GB:AE005673; NID:913421344; PIDN:AAK22204.1; GSPDB:GN00148	
A;Gene: CC0217	A;Gene: CC0217		A;Gene: APE0614	A;Gene: APE0614	
Query Match	15.1%; Score 76; DB 2; Length 699;		Query Match	15.0%; Score 75.5; DB 2; Length 544;	
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Matches	32; Conservative 18; Mismatches 37; Indels 18; Gaps 5;		Matches	33; Conservative 19; Mismatches 36; Indels 37; Gaps 5;	
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Db	545 VSMILGLLAATVGAALAAASALSXP---FVAAAALASTPSPGPLTAE---AWSPERKVOA	598	Db	18 ALVATAVAVAAALMSVGGERTAGIAGCEAAASSIAAASNPLXMEANVEAGA-----71	
Qy	62 SSLGIIVNHLIGS-----QKCAEALGPQAVGAVALKALL 97		Qy	51 LGTINPLKLSSLQIIPNHLI-----EGSQKCYVAELGPDAVGAVALK-----ALLGA 99	
Db	599 QAEGRPI-LVDETAACWTCQVNKEKVALSGPKVAAEAKRQNQAVL 641		Db	72 -----LKRYFYSPGAPVESVVVLKPGEVYARVLPPEAVEGVYDGYDCSPVILGV 125	
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C;Accession: T47269	C;Accession: T47269		Qy	100 LTVFG 104	
R.;Bayle, D.; Wangler, S.; Weitzneger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.; S.J. Bacteriol. 180, 317-329, 1998	R.;Bayle, D.; Wangler, S.; Weitzneger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.; S.J. Bacteriol. 180, 317-329, 1998		Db	126 ETVGG 130	
A;Title: Properties of the P-type ATPases encoded by the copAP operons of Helicobacter pylori	A;Title: Properties of the P-type ATPases encoded by the copAP operons of Helicobacter pylori		Qy	100 LTVFG 104	
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A;Molecule type: DNA	A;Molecule type: DNA		Db	126 ETVGG 130	
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A;Accession: T47269	A;Accession: T47269		Db	126 ETVGG 130	
A;Status: strain ATCC 49179	A;Status: strain ATCC 49179		Qy	100 LTVFG 104	
A;Keywords: copper binding; hydrolase	A;Keywords: copper binding; hydrolase		Db	126 ETVGG 130	
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F;532-674/Domain: Atpase nucleotide-binding domain homology <ATN>	F;532-674/Domain: Atpase nucleotide-binding domain homology <ATN>		Db	126 ETVGG 130	
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Best Local Similarity	26.3%; Pred. No. 22;		Best Local Similarity	27.9%; Pred. No. 17;	
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Qy	6 LIGLCAVALCSAAAFLVGSAKPVAPVAA-----BSAAEAGAG-----45		Qy	3 LAALIGLCAVALCSAAAFLVGSAKPVAPVAA-----BSAAEAGAG-----506	
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Qy	46 -TLANPLGTNPKLSSS---LGTVP-NHLLIESQKCYVAELGPQAVCA-----89		Qy	46 -TLANPLGTNPKLSSS---LGTVP-NHLLIESQKCYVAELGPQAVCA-----89	

Qy 63 SLG-----IPVNHLITEGSQKCVAELGPQAVGAVKALKALIGAL 100  
 Db 137 VLGSERTVPPLNFLRG-----VMSIRSIPALWAL 169

RESULT 11  
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 C;Species: Pseudomonas aeruginosa  
 C;Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
 C;Accession: F83553  
 R;Stover, K.C.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Br adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, J.; Lory, S.; Olson, M.V.  
 Nt:ature 406; 959-964, 2000  
 A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho gen  
 A;Reference number: A82950; MUID:20437337; PMID:10984043  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-502 <STO>  
 A;Cross-references: GB:AE004509; GB:AB004091; NID:9946622; PIDN:AG04136.1; GSPDB:GN001  
 A;Experimental source: strain PA01  
 C;Genetics:  
 A;Gene: PA047  
 C;Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology  
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 Best Local Similarity 29.1%; Pred. No. 29;  
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 Qy 4 AAILGLCYALCSSSA-----AAFLYNSAK---PAQPYVALESA---AEAGATL 47  
 Db 244 AQVGNLYASCGAGQRROMAISAVFVGAAREWIPEAERAVLPRPHQDPPDAAGPL 323  
 RESULT 14  
 A56010 amastigote-specific protein A2 precursor - Leishmania donovani infantum  
 Db 324 ISPOARQVRLLIAEGRAGEAECLLDGSQ-CQVEGPPNWILGPTLFFAV 372

Qy 48 ANPLGTLNPLKLUSSLGIPLVNLHIEGGSKVCAE-----LGPOQAVGAV 90  
 Db 372 ISPOARQVRLLIAEGRAGEAECLLDGSQ-CQVEGPPNWILGPTLFFAV

RESULT 12  
 B87315 gamma-glutamyltransferase [imported] - Caulobacter crescentus  
 C;Species: Caulobacter crescentus  
 C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
 C;Accession: B87315  
 R;Nieman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.B.; Eisen, J.; Heidelberg, J. B.; Laub, M.T.; DeBoy, R.T.; Douson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Ventre, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
 A;Title: Complete Genome Sequence of Caulobacter crescentus.  
 A;Reference number: A87249; MUID:21173698; PMID:11253647  
 A;Accession: B87315  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-584 <STO>  
 C;Superfamily: gamma-glutamyltransferase  
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 Db 7 RLASLIALSALQLSLAPVVALEAISTPLAMPTPRPAATSTPAKGMVAANPLAVEAGLRV 66

RESULT 15  
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 C;Species: Agrobacterium tumefaciens  
 C;Accession: AE2300  
 R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; We erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kuryaviv, T.; Levy, R.; Li, M.; McC

Qy 60 LISSSLGIPVNHLITEGSQKCVAELGPQAVGAVKALKAL 97  
 Db 67 LRD-----GASAVDAVAIQAVL 84

; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,  
ster, E. W.  
A; Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A; Reference number: AB2577; MUID:21608550; PMID:11743193  
A; Accession: AE2900  
A; Status: preliminary  
A; Molecule type: DNA  
A; Residues: 1-397 <KUR>  
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A; Experimental source: strain C58 (Dupont)  
C; Genetics:  
A; Gene: succC  
A; Map position: circular chromosome  
C; Superfamily: succinate CoA ligase (ADP-forming) beta chain  
Query Match 14.3%; Score 72; DB 2; Length 397;  
Best Local Similarity 36.2%; Pred. No. 28;  
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Db 8 AKALIKGYGAFAEGVALLKVEEAAAKQLPGLPVV--VKSQTHAGG-----RGKG 57  
Qy 77 KCVAELGPQAYGAVKALK 96  
Db 58 K-FKELGDAKGVRILAKSI 76

Search completed: June 2, 2004, 20:22:23  
Job time : 9.07942 secs

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2	502	100.0	104	9	US-09-989-723-408	Sequence 408, App	
3	502	100.0	104	9	US-09-989-729-408	Sequence 408, App	
4	502	100.0	104	9	US-09-989-727-408	Sequence 408, App	
5	502	100.0	104	9	US-09-989-731-408	Sequence 408, App	
6	502	100.0	104	9	US-09-989-732-408	Sequence 408, App	
7	502	100.0	104	9	US-09-991-073-408	Sequence 408, App	
8	502	100.0	104	9	US-09-990-442-408	Sequence 408, App	
9	502	100.0	104	9	US-09-991-163-408	Sequence 408, App	
10	502	100.0	104	9	US-09-993-604-408	Sequence 408, App	
11	502	100.0	104	9	US-09-990-456-408	Sequence 408, App	
12	502	100.0	104	9	US-09-989-721-408	Sequence 408, App	
13	502	100.0	104	9	US-09-992-598-408	Sequence 408, App	
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15	502	100.0	104	9	US-09-989-735-408	Sequence 408, App	

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1  
US-09-989-722-408  
; Sequence 408, Application US/09989722  
; Patent No. US2002072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Klijavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
; FILE REFERENCE: P2730P163  
; CURRENT APPLICATION NUMBER: US/09/989,722  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049757  
; PRIOR FILING DATE: 1997-06-16  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17

## ALIGNMENTS

PRIOR APPLICATION NUMBER: 60/065186  
PRIOR FILING DATE: 1997-11-12  
PRIOR APPLICATION NUMBER: 60/065311  
PRIOR FILING DATE: 1997-11-13  
PRIOR APPLICATION NUMBER: 60/066770  
PRIOR FILING DATE: 1997-11-24  
PRIOR APPLICATION NUMBER: 60/075945  
PRIOR FILING DATE: 1998-02-25  
PRIOR APPLICATION NUMBER: 60/078910  
PRIOR FILING DATE: 1998-03-20  
PRIOR APPLICATION NUMBER: 60/083322  
PRIOR FILING DATE: 1998-04-28  
PRIOR APPLICATION NUMBER: 60/084600  
PRIOR FILING DATE: 1998-05-07  
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PRIOR FILING DATE: 1998-05-28  
PRIOR APPLICATION NUMBER: 60/087607  
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PRIOR APPLICATION NUMBER: 60/087609  
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PRIOR APPLICATION NUMBER: 60/087759  
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PRIOR FILING DATE: 1998-06-03  
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PRIOR APPLICATION NUMBER: 60/088025  
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PRIOR FILING DATE: 1998-07-01  
PRIOR APPLICATION NUMBER: 60/091478  
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PRIOR APPLICATION NUMBER: 60/091544  
PRIOR FILING DATE: 1998-07-01  
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PRIOR FILING DATE: 1998-07-02  
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PRIOR FILING DATE: 1998-07-02  
PRIOR APPLICATION NUMBER: 60/091978  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/091982  
PRIOR FILING DATE: 1998-07-07  
PRIOR APPLICATION NUMBER: 60/092182  
PRIOR FILING DATE: 1998-07-09

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Best Local Similarity 100.0%; Pred. No. 7.5e-47; Mismatches 0; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLAALLGCVLSCSSAAAFLVGSAKPVQALESAAAGAGTLANPLGTNPLKL 60

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Db 61 LSSLGIPVNHLLEGSKRCVNLGPQAVGAVALKALLGLALTVG 104

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RESULT 2 US-09-989-723-08  
Sequence 408, Application US/09989723  
Patent No. US2002072092A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paponi, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William T.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730PC62  
CURRENT APPLICATION NUMBER: US/09/989,723  
CURRENT FILING DATE: 2001-11-19  
PRIOR APPLICATION NUMBER: 60/049787  
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 PRIOR APPLICATION NUMBER: 60/091478

Query Match 100.0%; Score 502; DB 9; Length 104;  
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 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 LSSLGIPVNHLLEGSGQRCKVQELGPQAVGAYKALKGALTGVFG 104  
 Db 61 LSSLGIPVNHLLEGSGQRCKVQELGPQAVGAYKALKGALTGVFG 104

RESULT 3  
 US-09-989-279-408  
 Sequence 408, Application US/099893279  
 Patent No. US20020072436A1

GENERAL INFORMATION:  
 / APPLICANT: Ashkenazi Avi J.  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hans Peter  
 / APPLICANT: Gerittsen, Mary E.  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Grimaldi, J. Christopher  
 / APPLICANT: Guirney Austin L.  
 / APPLICANT: Klijavin, Ivar J.  
 / APPLICANT: Pan, James  
 / APPLICANT: Pacini, Nicholas F.  
 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Colin K.  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P7301PC6  
 CURRENT APPLICATION NUMBER: US/09/989,279  
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 / PRIOR FILING DATE: 1997-06-16  
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 / PRIOR FILING DATE: 1997-11-13  
 / PRIOR APPLICATION NUMBER: 60/066770  
 / PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945  
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match Similarity 100.0%; Score 502; DB 9; Length 104;  
 Matches 104; Conservative 0; Mismatches 0; Gaps 0;

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**RESULT 4**  
 US-09-989-727-408  
 Sequence 408, Application US/0989727  
 Patent No. US20020072497A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Debnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kjavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same  
 FILE REFERENCE: P2730P1C65  
 CURRENT APPLICATION NUMBER: US/09/989,727  
 CURRENT FILING DATE: 2001-11-19  
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Best Local Similarity 100 :0% ; Pred. No. 7.5e-47;
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RESULT 5
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; Sequence 408, Application US/09989731
; Patent No. US20020103125A1
; GENERAL INFORMATION:
;   APPLICANT: Ashkenazi, Avi J.
;   APPLICANT: Baker, Kevin P.
;   APPLICANT: Botstein, David
;   APPLICANT: Desnoyers, Luc
;   APPLICANT: Eaton, Dan L.
;   APPLICANT: Ferrara, Napoleone
;   APPLICANT: Fong, Sherman
;   APPLICANT: Gerber, Hanspeter
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;   APPLICANT: Godowski, Paul J.
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;   APPLICANT: Paoni, Nicholas F.
;   APPLICANT: Roy, Margaret Ann
;   APPLICANT: Stewart, Timothy A.
;   APPLICANT: Thomas, Daniel
;   APPLICANT: Watanabe, Colin K.
;   APPLICANT: Williams, P. Mickey
;   APPLICANT: Wood, William I.
;   APPLICANT: Zeman, Zhenan

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC70
; CURRENT APPLICATION NUMBER: US/091989_731
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; PRIOR FILING DATE: 1998-07-02
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 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/091982  
 PRIOR FILING DATE: 1998-07-07  
 PRIOR APPLICATION NUMBER: 60/092182  
 PRIOR FILING DATE: 1998-07-09

Query Match Similarity: 100.0%; Score: 502; DB: 9; Length: 104;  
 Best Local Similarity: 100.0%; Pred. No.: 7.5e-47; Indels: 0; Gaps: 0;  
 Matches: 104; Conservative: 0; Mismatches: 0;

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Qy 61 LSSIGIPVNHLIESSQKCVAELGPQAVGVAKKALLGALTVFG 104  
 Db 61 LSSIGIPVNHLIESSQKCVAELGPQAVGVAKKALLGALTVFG 104

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RESULT 6

US-09-989-722-408  
 Sequence: 408, Application US/09989732  
 Patent No. US200212463A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Deanoers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurley, Austin L.  
 APPLICANT: Kliavir, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Thomas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William T.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P27310P1C57

CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/043787  
 PRIOR FILING DATE: 1997-06-16  
 PRIOR APPLICATION NUMBER: 60/062250  
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; PRIOR FILING DATE: 1998-07-09

Query Match Score 502; DB 9; Length 104;
Best Local Similarity 100.0%; Pred. No. 7.5e-47;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 7
US-09-991-073-408 ; Sequence 408, Application US/0991073
; Patent No. US2002012576A1

; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Debroyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: DeBruyn, Audrey
; APPLICANT: Goddard, Andrej
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Guiney, Austin L.
; APPLICANT: Klijavins, Ivar J.
; APPLICANT: Naper, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; APPLICANT: Acids Encoding the Same
; FILE REFERENCE: P2730PIC15
; CURRENT APPLICATION NUMBER: US/09/991,073
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PRIOR FILING DATE: 1998-06-17  
PRIOR APPLICATION NUMBER: 60/089801  
PRIOR FILING DATE: 1998-06-18  
PRIOR APPLICATION NUMBER: 60/089807  
PRIOR FILING DATE: 1998-06-18

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Qy      61    LSSLGIPVNHLLEGSKOKCVAELGPQAVGAVKALKALIGALTIVFG 104  
 Db      61    LSSLGIPVNHLLEGSKQCVAELGPQAVGAVKALKALIGALTIVFG 104

RESULT 8  
 US-09-990-442-408  
 / Sequence 408, Application US/09990442  
 / GENERAL INFORMATION:  
 /    APPLICANT: Ashkenazi, Avi J.  
 /    APPLICANT: Baker, Kevin P.  
 /    APPLICANT: Botstein, David  
 /    APPLICANT: Desnoyers, Luc  
 /    APPLICANT: Eaton, Dan L.  
 /    APPLICANT: Ferrara, Napoleone  
 /    APPLICANT: Fong, Sherman  
 /    APPLICANT: Gerber, Hanspeter  
 /    APPLICANT: Gerritsen, Mary E.  
 /    APPLICANT: Goddard, Audrey  
 /    APPLICANT: Godowski, Paul J.  
 /    APPLICANT: Grimaldi, J. Christopher  
 /    APPLICANT: Gurney, Austin L.  
 /    APPLICANT: Kijariv, Iivar J.  
 /    APPLICANT: Napier, Mary A.  
 /    APPLICANT: Pan, James  
 /    APPLICANT: Paoni, Nicholas F.  
 /    APPLICANT: Roy, Margaret Ann  
 /    APPLICANT: Stewart, Timothy A.  
 /    APPLICANT: Tomas, Daniel  
 /    APPLICANT: Watanabe, Colin K.  
 /    APPLICANT: Williams, P. Mickey  
 /    APPLICANT: Wood, William J.

/ TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same  
 FILE REFERENCE: P273D1CB  
 CURRENT APPLICATION NUMBER: US/09/990,442  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR APPLICATION NUMBER: 60/052250  
 PRIOR APPLICATION NUMBER: 1997-10-17  
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 PRIOR FILING DATE: 1998-07-01

Query Match 100.0% Score 502; DB 9; Length 104;  
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Matches 104; Conservative 0; Mismatches 0; Indexes 0; Gaps 0;

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QY 61 LSSLGIPVNHLIEGSQKCVTAELGQAVGAKVAKLALLGALTVEG 104  
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RESULT 9  
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 Patent No. US200513253A1

GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desboyez, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleon  
 APPLICANT: Fong, Sherman  
 APPLICANT: Gerber, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
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 APPLICANT: Godowski, Paul J.  
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 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tummas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

CURRENT APPLICATION NUMBER: US/09/991,163  
 CURRENT FILING DATE: 2001-11-14  
 FILE REFERENCE: P2730P1C17

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Query Match          100.0% ; Score 502; DB 9; Length 104;
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 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Botstein, David  
 / APPLICANT: Desnoyers, Luc  
 / APPLICANT: Eaton, Dan L.  
 / APPLICANT: Ferrara, Napoleone  
 / APPLICANT: Fong, Sherman  
 / APPLICANT: Gerber, Hans Peter  
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 / APPLICANT: Roy, Margaret Ann  
 / APPLICANT: Stewart, Timothy A.  
 / APPLICANT: Tumas, Daniel  
 / APPLICANT: Watanabe, Colin K.  
 / APPLICANT: Williams, P. Mickey  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin  
 / TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acids Encoding the Same  
 / TITLE OF INVENTION: Acids Encoding the Same  
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Db 61 LSSGLIPVNLIESSQKCVYAEGLGQAAGVAKALKALLGALTIVFG 104

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RESULT 12

US-09-989-721-408, Application US/09989721  
 Sequence 408, Application US/09989721  
 Patent No. US20020142961A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Borstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

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APPLICANT: Klijavc, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

TITLE OF INVENTION: Secreted and Transmembrane polypeptides and Nucleic FILE REFERENCE: P2730PIC55

CURRENT FILING DATE: 2001-11-19

PRIOR APPLICATION NUMBER: 60/049787

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PRIOR FILING DATE: 1998-07-09

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US-09-992-598-408 Application US/09992598  
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; Patent No. US20020103841  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
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; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gerritsen, Mary E.  
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; APPLICANT: Godowski, Paul J.  
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; APPLICANT: Tumans, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; ACIDS Encoding the Same  
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RESULT 14
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; Sequence 408, Application US/09589293A
; Patent No. US200201771641

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GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Boiststein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber-Hanspetter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Klijavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tuma, Daniel

APPLICANT: Watanabe, Colin X.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William J.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Acid Encoding the Same

FILE REFERENCE: P2730P1C66

CURRENT APPLICATION NUMBER: US/09/989,293A

CURRENT FILING DATE: 2001-11-20

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

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 ; Publication No. US2002013299A1  
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 ; APPLICANT: Ashekazi, Avi J.  
 ; APPLICANT: Baker, Kevin P.

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 / PRIOR FILING DATE: 1998-06-25  
 / PRIOR APPLICATION NUMBER: 60/090862  
 / PRIOR FILING DATE: 1998-06-26  
 / PRIOR APPLICATION NUMBER: 60/090863  
 / PRIOR FILING DATE: 1998-06-26  
 / PRIOR APPLICATION NUMBER: 60/091360  
 / PRIOR FILING DATE: 1998-07-01  
 / PRIOR APPLICATION NUMBER: 60/091478  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091544  
 / PRIOR FILING DATE: 1998-07-01  
 / PRIOR APPLICATION NUMBER: 60/091519  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/09126  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091633  
 / PRIOR FILING DATE: 1998-07-02  
 / PRIOR APPLICATION NUMBER: 60/091978  
 / PRIOR FILING DATE: 1998-07-07  
 / PRIOR APPLICATION NUMBER: 60/091982  
 / PRIOR FILING DATE: 1998-07-07  
 / PRIOR APPLICATION NUMBER: 60/092182  
 / PRIOR FILING DATE: 1998-07-09

Query Match 100.0%; Score 502; DB 9; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 7.5e-17;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLALLGLCVALSQSSAAFLVGSAKEVQPVALEAEGAGTLANPLGTINPLKLL 60  
 Db 1 MKLALLGLCVALSQSSAAFLVGSAKEVQPVALEAEGAGTLANPLGTINPLKLL 60

Qy 61 LSSLGIPYVNLHLSQKCVAEILGQAVGAKVALIGALITYFG 104  
 Db 61 LSSLGIPYVNLHLSQKCVAEILGQAVGAKVALIGALITYFG 104

Search completed: June 2, 2004, 20:25:21  
 Job time : 20.5413 SECs

Gencore version 5.1.6  
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OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 7.24797 Seconds  
 (without alignments) Million cell updates/sec  
 740.773

Title: US-09-700-770-9

Perfect score: 502

Sequence: 1 MKLAAALIGCVALSQSSAAA.....QAVGAVKALKALLGALTGVFG 104

Scoring table: BLOSUM62

Gapext: 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 100%  
 Listing first 45 summaries

Database : Issued Patents AA:  
 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:  
 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:  
 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep:  
 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:  
 5: /cgn2\_6/ptodata/2/iaa/PCT05.COMB.pep:  
 6: /cgn2\_6/ptodata/2/iaa/backfile1.pep:  
 \*

Prev. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	160	31.9	93	2	US-09-964-725-14
2	83	16.5	673	3	US-09-196-387-9
3	83	16.5	673	4	US-09-841-835-8
4	83	16.5	83	3	US-09-196-387-10
5	83	16.5	949	4	US-09-841-835-10
6	83	16.5	1327	3	US-09-195-387-2
7	83	16.5	1327	4	US-09-841-835-2
8	83	16.5	1327	4	US-09-972-115A-8
9	82.5	16.4	718	4	US-09-252-991A-25696
10	78.5	15.6	255	4	US-09-252-991A-21756
11	77	15.3	540	4	US-09-252-991A-29143
12	73.5	14.6	443	3	US-09-08B-425-2
13	73.5	14.6	477	2	US-09-639-378A-2
14	73.5	14.6	477	4	US-09-523-849-34
15	72	14.3	236	1	US-08-452-331-3
16	72	14.3	236	1	US-08-460-746A-3
17	72	14.3	236	2	US-08-460-555-3
18	72	14.3	236	2	US-08-460-666-3
19	69.5	13.8	423	3	US-09-073-009-142
20	69.5	13.8	423	4	US-09-073-010-142
21	69.5	13.8	856	4	US-09-287-849-16
22	69	13.8	856	4	US-09-287-849-12
23	69	13.7	468	4	US-09-252-991A-28114
24	68.5	13.6	163	4	US-09-252-991A-22281
25	68	13.5	461	4	US-08-194-338-4
26	68	13.5	480	4	US-09-143-661A-4680
27	67	13.3	419	4	US-09-252-991A-26821

## ALIGNMENTS

RESULT 1  
 US-09-964-725-14  
 Sequence 14, Application US/08964725  
 Patent No. 5939265

GENERAL INFORMATION:

APPLICANT: COHEN, Maurice  
 APPLICANT: FRIEDMAN, Paula N.  
 APPLICANT: GORDON, Julian  
 APPLICANT: HONGES, Steven C.  
 APPLICANT: KLAAS, Michael R.  
 APPLICANT: KRATOCHVIL, Jon D.  
 APPLICANT: ROBERTS-RAPP, Lisa  
 APPLICANT: ROSELLI, John C.  
 APPLICANT: STROUP, Steven D.  
 APPLICANT: STROUSE, Steven D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE LUNG

NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:

ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS

SOFTWARE: FABSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/964,725  
 FILING DATE: 14-06-2008  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Becker, Cheryl L.  
 REGISTRATION NUMBER: 35,441  
 REFERENCE/DOCKET NUMBER: 5997.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 847/935-7729  
 TELEFAX: 847/938-2673

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 93 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: Linear

RESULT 3  
 US-09-841-835-B  
 Sequence 8, Application US/09841835  
 Patent No. 6506587  
 GENERAL INFORMATION:  
 APPLICANT: de Lange, Titia  
 TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue, 4th Floor  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/841,835  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/196,387  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-230 CIP1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 TELE: 133521  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 673 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-841-835-B

Query Match Score 83; DB 4; Length 673;  
 Best Local Similarity 30.5%; Pred. No. 0.28;  
 Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

Qy 1 MKKAAALLQLCVALSCS-SAAAFLYGSAKPVAAQPVAALESAA----ENGAGTIANPGLTLNPKLILSIGIPVN 69  
 Db 1 MKLVTVIILVLTISLCVSYATFLINKVLPDKLAPL-----PLDNIDPFMDBLKL 51

60 LLLSLGIVPNHLLLEGSQLCKVVAELGPQAVGAVKALKALGAL 100  
 Qy 52 LLKTIGISVHEVLVEGLRVCNELLGEASEAVKXKLEALSHL 92  
 Db 52

---

RESULT 2  
 US-09-196-387-8  
 Sequence 8, Application US/09196387  
 Patent No. 6277613  
 GENERAL INFORMATION:  
 APPLICANT: de Lange, Titia  
 APPLICANT: Smith, Susan  
 TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue, 4th Floor  
 CITY: Hackensack  
 STATE: New Jersey  
 COUNTRY: USA  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/196,387  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/196,387  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-230 CIP1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 TELE: 133521  
 INFORMATION FOR SEQ ID NO: 8:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 673 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-196-387-8

Query Match Score 83; DB 4; Length 673;  
 Best Local Similarity 30.5%; Pred. No. 0.28;  
 Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

Qy 15 CSSAAAFLYGSAKPVAAQPVAALESAA----EAGAGTIANPGLTNPKLILSIGIPVN 69  
 Db 90 CSTSTCTVAAAPVY-PAVTSAAAGVAPNPGSGNNSPSSSSPTSSSSSPSPGS 148

70 HLLEGSQ---KCVAELGPQAVGAVKALKALGAL 100  
 Qy 149 SLAESPEAGVSSSTAPLGPGAGPTGVPAVGAL 183  
 Db

---

RESULT 4  
 US-09-196-387-10  
 Sequence 10, Application US/09196387  
 Patent No. 6277613  
 GENERAL INFORMATION:  
 APPLICANT: de Lange, Titia  
 APPLICANT: Smith, Susan  
 TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue, 4th Floor  
 CITY: Hackensack

STATE: New Jersey  
 COUNTRY: USA  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/196,387  
 FILING DATE:  
 CLASIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/095,225  
 FILING DATE: June 10, 1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-230 CIP1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 INSTRUCTION FOR SEQ ID NO: 10:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 949 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-196-387-10

Query Match 16.5%; Score 83; DB 4; Length 949;  
 Best Local Similarity 30.5%; Pred. No. 0.45; Indels 10; Gaps 3;  
 Matches 29; Conservative 13; Mismatches 43; Gaps 3;

Qy 15 CSSAAAFLVGSAKPVAAQPVVALESA--BAGAGTIANPLGTLNPLKLISSLGIPVN 69  
 Db 90 CSTTSTICTVAAAPVV-PAVSTSSAAVGAVPNPGSGNSNPSSSSPTSSSSSPSPGS 148

Qy 70 HLIJEGSQ---KCVAAELPQAVGAVKALKALCAL 100  
 Db 149 SLAESPERAGVSSTAPLPGANGPGTGYPAVSGAL 183

RESULT 5  
 US-09-041-835-10  
 Sequence 10, Application US/09841835  
 Patent No. 6505587  
 GENERAL INFORMATION:  
 APPLICANT: de Lange, Titia  
 ATTORNEY/AGENT INFORMATION:  
 APPLICANT: Smith, Susan  
 TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS  
 NUMBER OF SEQUENCES: 12  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Klauber & Jackson  
 STREET: 411 Hackensack Avenue, 4th Floor  
 CITY: Hackensack  
 STATE: New Jersey  
 ZIP: 07601  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/196,387  
 FILING DATE:  
 CLASIFICATION:  
 PRIOR APPLICATION DATA:  
 FILING DATE: June 10, 1998  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Jackson Esq., David A.  
 REGISTRATION NUMBER: 26,742  
 REFERENCE/DOCKET NUMBER: 600-1-230 CIP1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-487-5800  
 TELEFAX: 201-343-1684  
 INSTRUCTION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1327 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FILING DATE:

CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 09/196,387  
 FILING DATE:

; HYPOTHETICAL: NO  
 US-09-196-387-2

Query Match 16.5%; Score 83; DB 3; Length 1327;  
 Best Local Similarity 30.5%; Pred. No. 0.71;  
 Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

Qy 15 C<sub>5</sub>S<sub>3</sub>A<sub>2</sub>A<sub>1</sub>F<sub>1</sub>V<sub>2</sub>G<sub>3</sub>A<sub>4</sub>K<sub>5</sub>P<sub>6</sub>V<sub>7</sub>A<sub>8</sub>E<sub>9</sub>S<sub>10</sub>A<sub>11</sub>---BAGAGT<sub>12</sub>L<sub>13</sub>A<sub>14</sub>P<sub>15</sub>T<sub>16</sub>N<sub>17</sub>P<sub>18</sub>K<sub>19</sub>L<sub>20</sub>I<sub>21</sub>S<sub>22</sub>L<sub>23</sub>G<sub>24</sub>I<sub>25</sub>P<sub>26</sub>V<sub>27</sub>N<sub>28</sub> 69  
 Db 90 C<sub>5</sub>T<sub>4</sub>S<sub>3</sub>T<sub>2</sub>C<sub>1</sub>T<sub>1</sub>V<sub>2</sub>A<sub>3</sub>P<sub>4</sub>V<sub>5</sub>A<sub>6</sub>V<sub>7</sub>T<sub>8</sub>S<sub>9</sub>S<sub>10</sub>A<sub>11</sub>G<sub>12</sub>Y<sub>13</sub>A<sub>14</sub>P<sub>15</sub>G<sub>16</sub>S<sub>17</sub>N<sub>18</sub>S<sub>19</sub>P<sub>20</sub>S<sub>21</sub>P<sub>22</sub>G<sub>23</sub>S<sub>24</sub> 148

Qy 70 H<sub>1</sub>L<sub>2</sub>I<sub>3</sub>E<sub>4</sub>G<sub>5</sub>S<sub>6</sub>Q<sub>7</sub>A<sub>8</sub>V<sub>9</sub>G<sub>10</sub>A<sub>11</sub>K<sub>12</sub>A<sub>13</sub>L<sub>14</sub>G<sub>15</sub> 100  
 Db 149 S<sub>1</sub>L<sub>2</sub>A<sub>3</sub>E<sub>4</sub>S<sub>5</sub>P<sub>6</sub>R<sub>7</sub>A<sub>8</sub>G<sub>9</sub>V<sub>10</sub>S<sub>11</sub>T<sub>12</sub>A<sub>13</sub>P<sub>14</sub>L<sub>15</sub>G<sub>16</sub>P<sub>17</sub>G<sub>18</sub>A<sub>19</sub>G<sub>20</sub>T<sub>21</sub>G<sub>22</sub>V<sub>23</sub>P<sub>24</sub>S<sub>25</sub>G<sub>26</sub>A<sub>27</sub> 183

RESULT 7  
 US-09-841-835-2

; Sequence 2, Application US/09841835  
 ; Patent No. 650587

; GENERAL INFORMATION:  
 ; APPLICANT: de Lange, Titia  
 ; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS  
 ; TITLE OF INVENTION: OF USE THEREOF  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Klauter & Jackson  
 ; STREET: 411 Hackensack Avenue, 4th Floor  
 ; CITY: Hackensack  
 ; STATE: New Jersey  
 ; COUNTRY: USA  
 ; ZIP: 07601  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.3.0  
 ; CURRENT APPLICATION NUMBER: US/09/841, 835  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 09/196, 387  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Jackson, Esq., David A.  
 ; REGISTRATION NUMBER: 26, 742  
 ; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 201-487-5800  
 ; TELEFAX: 201-343-1684  
 ; TELEX: 133521  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1327 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; HYPOTHETICAL: NO  
 ; US-09-841-835-2

Query Match 16.5%; Score 83; DB 4; Length 1327;  
 Best Local Similarity 30.5%; Pred. No. 0.71;  
 Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

Qy 15 C<sub>5</sub>S<sub>3</sub>A<sub>2</sub>A<sub>1</sub>F<sub>1</sub>V<sub>2</sub>G<sub>3</sub>A<sub>4</sub>K<sub>5</sub>P<sub>6</sub>V<sub>7</sub>A<sub>8</sub>E<sub>9</sub>S<sub>10</sub>A<sub>11</sub>---BAGAGT<sub>12</sub>L<sub>13</sub>A<sub>14</sub>P<sub>15</sub>T<sub>16</sub>N<sub>17</sub>P<sub>18</sub>K<sub>19</sub>L<sub>20</sub>I<sub>21</sub>S<sub>22</sub>L<sub>23</sub>G<sub>24</sub>I<sub>25</sub>P<sub>26</sub>V<sub>27</sub>N<sub>28</sub> 69  
 Db 90 C<sub>5</sub>T<sub>4</sub>S<sub>3</sub>T<sub>2</sub>C<sub>1</sub>T<sub>1</sub>V<sub>2</sub>A<sub>3</sub>P<sub>4</sub>V<sub>5</sub>A<sub>6</sub>V<sub>7</sub>T<sub>8</sub>S<sub>9</sub>S<sub>10</sub>A<sub>11</sub>G<sub>12</sub>Y<sub>13</sub>A<sub>14</sub>P<sub>15</sub>G<sub>16</sub>S<sub>17</sub>N<sub>18</sub>S<sub>19</sub>P<sub>20</sub>S<sub>21</sub>P<sub>22</sub>G<sub>23</sub>S<sub>24</sub> 148

Qy 70 H<sub>1</sub>L<sub>2</sub>I<sub>3</sub>E<sub>4</sub>G<sub>5</sub>S<sub>6</sub>Q<sub>7</sub>A<sub>8</sub>V<sub>9</sub>G<sub>10</sub>A<sub>11</sub>K<sub>12</sub>A<sub>13</sub>L<sub>14</sub>G<sub>15</sub> 100

Db Db 149 S<sub>1</sub>A<sub>2</sub>L<sub>3</sub>E<sub>4</sub>S<sub>5</sub>P<sub>6</sub>R<sub>7</sub>A<sub>8</sub>G<sub>9</sub>V<sub>10</sub>S<sub>11</sub>T<sub>12</sub>A<sub>13</sub>P<sub>14</sub>L<sub>15</sub>G<sub>16</sub>P<sub>17</sub>G<sub>18</sub>A<sub>19</sub>G<sub>20</sub>T<sub>21</sub>G<sub>22</sub>V<sub>23</sub>P<sub>24</sub>S<sub>25</sub>G<sub>26</sub>A<sub>27</sub> 183

RESULT 8  
 US-09-972-115A-8

; Sequence 8, Application US/09972115A  
 ; Patent No. 659728

; GENERAL INFORMATION:  
 ; APPLICANT: Geron Corporation  
 ; APPLICANT: Gregg, Morin B.  
 ; APPLICANT: Walter, Funk B.  
 ; APPLICANT: Mieczyslaw, Piatszsek A.  
 ; TITLE OF INVENTION: A Second Mammalian Telomerase  
 ; FILE REFERENCE: 080/003C  
 ; CURRENT APPLICATION NUMBER: US/09/972,115A  
 ; CURRENT FILING DATE: 2000-10-05  
 ; PRIORITY NUMBER: US 60/128, 577  
 ; PRIORITY FILING DATE: 2000-04-10  
 ; PRIORITY APPLICATION NUMBER: US 60/129, 123  
 ; PRIORITY FILING DATE: 1999-04-13  
 ; NUMBER OF SEQ ID NOS: 64  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO: 8

Query Match 16.5%; Score 83; DB 4; Length 1327;  
 Best Local Similarity 30.5%; Pred. No. 0.71;  
 Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

Qy 15 C<sub>5</sub>S<sub>3</sub>A<sub>2</sub>A<sub>1</sub>F<sub>1</sub>V<sub>2</sub>G<sub>3</sub>A<sub>4</sub>K<sub>5</sub>P<sub>6</sub>V<sub>7</sub>A<sub>8</sub>E<sub>9</sub>S<sub>10</sub>A<sub>11</sub>---BAGAGT<sub>12</sub>L<sub>13</sub>A<sub>14</sub>P<sub>15</sub>T<sub>16</sub>N<sub>17</sub>P<sub>18</sub>K<sub>19</sub>L<sub>20</sub>I<sub>21</sub>S<sub>22</sub>L<sub>23</sub>G<sub>24</sub>I<sub>25</sub>P<sub>26</sub>V<sub>27</sub>N<sub>28</sub> 69  
 Db 90 C<sub>5</sub>T<sub>4</sub>S<sub>3</sub>T<sub>2</sub>C<sub>1</sub>T<sub>1</sub>V<sub>2</sub>A<sub>3</sub>P<sub>4</sub>V<sub>5</sub>A<sub>6</sub>V<sub>7</sub>T<sub>8</sub>S<sub>9</sub>S<sub>10</sub>A<sub>11</sub>G<sub>12</sub>Y<sub>13</sub>A<sub>14</sub>P<sub>15</sub>G<sub>16</sub>S<sub>17</sub>N<sub>18</sub>S<sub>19</sub>P<sub>20</sub>S<sub>21</sub>P<sub>22</sub>G<sub>23</sub>S<sub>24</sub> 148

Qy 70 H<sub>1</sub>L<sub>2</sub>I<sub>3</sub>E<sub>4</sub>G<sub>5</sub>S<sub>6</sub>Q<sub>7</sub>A<sub>8</sub>V<sub>9</sub>G<sub>10</sub>A<sub>11</sub>K<sub>12</sub>A<sub>13</sub>L<sub>14</sub>G<sub>15</sub> 100  
 Db 149 S<sub>1</sub>A<sub>2</sub>L<sub>3</sub>E<sub>4</sub>S<sub>5</sub>P<sub>6</sub>R<sub>7</sub>A<sub>8</sub>G<sub>9</sub>V<sub>10</sub>S<sub>11</sub>T<sub>12</sub>A<sub>13</sub>P<sub>14</sub>L<sub>15</sub>G<sub>16</sub>P<sub>17</sub>G<sub>18</sub>A<sub>19</sub>G<sub>20</sub>T<sub>21</sub>G<sub>22</sub>V<sub>23</sub>P<sub>24</sub>S<sub>25</sub>G<sub>26</sub>A<sub>27</sub> 183

RESULT 9  
 US-09-252-991A-25696

; Sequence 25696, Application US/09252991A  
 ; Patent No. 6551/95

; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenstein et al.  
 ; TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO PSUEDOMONAS  
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
 ; FILE REFERENCE: 107196.1336  
 ; CURRENT APPLICATION NUMBER: US/09/252, 991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIORITY NUMBER: US 60/074, 788  
 ; PRIORITY FILING DATE: 1998-02-18  
 ; PRIORITY APPLICATION NUMBER: US 60/094, 190  
 ; PRIORITY FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO: 25696  
 ; LENGTH: 718  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-25696

Query Match 16.5%; Score 83; DB 4; Length 718;  
 Best Local Similarity 37.3%; Pred. No. 0.35;  
 Matches 25; Conservative 8; Mismatches 31; Indels 3; Gaps 2;

Qy 15 C<sub>5</sub>S<sub>3</sub>A<sub>2</sub>A<sub>1</sub>F<sub>1</sub>V<sub>2</sub>G<sub>3</sub>A<sub>4</sub>K<sub>5</sub>P<sub>6</sub>V<sub>7</sub>A<sub>8</sub>E<sub>9</sub>S<sub>10</sub>A<sub>11</sub>---GAGAGT<sub>12</sub>L<sub>13</sub>A<sub>14</sub>P<sub>15</sub>T<sub>16</sub>N<sub>17</sub>P<sub>18</sub>K<sub>19</sub>L<sub>20</sub>I<sub>21</sub>S<sub>22</sub>L<sub>23</sub>G<sub>24</sub>I<sub>25</sub>P<sub>26</sub>V<sub>27</sub>N<sub>28</sub> 69  
 Db 139 G<sub>1</sub>C<sub>2</sub>A<sub>3</sub>L<sub>4</sub>G<sub>5</sub>Q<sub>6</sub>A<sub>7</sub>F<sub>8</sub>Q<sub>9</sub>V<sub>10</sub>D<sub>11</sub>G<sub>12</sub>R<sub>13</sub>Y<sub>14</sub>L<sub>15</sub>Q<sub>16</sub>Q<sub>17</sub>R<sub>18</sub>V<sub>19</sub>A<sub>20</sub>G<sub>21</sub>D<sub>22</sub>E<sub>23</sub>G<sub>24</sub>A<sub>25</sub>Q<sub>26</sub>D<sub>27</sub>A<sub>28</sub> 147

Qy 82 L<sub>1</sub>G<sub>2</sub>P<sub>3</sub>A<sub>4</sub>V<sub>5</sub>G<sub>6</sub> 88

Db 198 AGFGALG 204

RESULT 10  
 US-09-252-991A-21756  
 ; Sequence 21756, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 1071.96.1136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO: 21756  
 ; LENGTH: 255  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-21756

Query Match 15.6%; Score 78.5; DB 4; Length 255;  
 Best Local Similarity 24.1%; Pred. No. 0.25; Indels 71; Gaps 6;  
 Matches 39; Conservative 10; Mismatches 42; GTLANPLGTINPLK 58  
 Qy 10 CVALCSSSA-AAFLYGSAKPVAQPVAALESAAEAGA-GTLANPLGTINPLK 58  
 Db 7 CLAAECCAAHPAAFDGCRGPVVRAGEAFRSAVEAGVQADLVEHLYGRATGLGLVGD-- 64  
 Qy 59 LLISSLGGIPVNH-----LIEG-----74  
 Db 65 -LLEGLRVPRPHARPEHQVHGSDGETTVGLDGAGLDTGQAGLAEEHRQHAEAA 123  
 Qy 75 -----SQRKVAAELGPAAVGAV-KALKALLGALTFV 103  
 Db 124 GVGRADOLFRRVGSRCALEFAAGVYLLERAFFGGKGALAVF 165

RESULT 11  
 US-09-252-991A-29143  
 ; Sequence 29143, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 1071.96.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO: 29143  
 ; LENGTH: 540  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 ; US-09-252-991A-29143

Query Match 15.3%; Score 77; DB 4; Length 540;  
 Best Local Similarity 30.0%; Pred. No. 1.1; Mismatches 40; Indels 24; Gaps 5;

Qy 4 AATIGLCVALCSSSA-----AAFLYGSAK----PVAQPVALESA---ABAGACTL 47

Db 302 AQVLGNLNVGASCAGAQRGMAISAVFVAAREMIPPELMARPHWQDFDAAYCPL 361

Qy 48 ANPLGTLNPIKLSSLSIIPVNHLJEGSQXCVAE-----LGFAQVAV 90

Db 380 SETRAQAGGGACVAELIGPLELVG 404

RESULT 13  
 US-09-639-378A-2  
 ; Sequence 2, Application US/09639378A  
 ; Patent No. 6522838  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga

Db 362 ISPARQRVRLIAEGKAEGAECULDGSQ-CQVEGYPNGNWLGPFLFRV 410  
 RESULT 12  
 US-09-088-425-2  
 ; Sequence 2, Application US/09088425  
 ; Patent No. 617143  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BANDMAN, OLGA  
 ; APPLICANT: LAL, PREETI  
 ; APPLICANT: CORLEY, NEIL C.  
 ; APPLICANT: PATTERSON, CHANDRA  
 ; APPLICANT: BRAGHAN, MARIAH R.  
 ; TITLE OF INVENTION: HUMAN ISOMERASE-LIKE PROTEINS  
 ; NUMBER OF SEQUENCE: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3114 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0b  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/088,425  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER:  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Carrone, Michael C  
 ; REGISTRATION NUMBER: 39,132  
 ; REFERENCE/DOCKET NUMBER: PF-0529 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; TELEX:  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQENCE CHARACTERISTICS:  
 ; LENGTH: 443 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: Single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: TMLR3DT01  
 ; CLONE: 289973  
 ; US-09-088-425-2  
 Query Match 14.6%; Score 73.5; DB 3; Length 443;  
 Best Local Similarity 34.1%; Pred. No. 2.1; Mismatches 26; Indels 21; Gaps 4;  
 Matches 29; Conservative 9; Missmatches 26; Indels 21; Gaps 4;  
 Qy 35 ALSEAEEAGACTANPILGTNLK-----LIGIPVNHLJEGSQXCV 79  
 Db 326 ALBEBALCG-----QSILGPVEPLDGPAGAVLBCLVSSGMLVPELAIPVVVIL-GALTML 379  
 Qy 80 ABIGPORVAGVAKALKALIGATVFG 104  
 Db 380 SETRAQAGGGACVAELIGPLELVG 404

RESULT 15  
US-09-452-531-3  
Sequence 3, Application US/08452531  
Patent No. 5733778  
GENERAL INFORMATION:  
APPLICANT: MATLASHIEWSKI, Gregory  
APPLICANT: CHARBET, Hughes  
TITLE OF INVENTION: GENES OF LEISHMANIA WHICH ARE DIFFERENTIALLY-  
EXRESSED IN ANASTIGOTE FORM  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sim & McBurney  
STREET: Suite 701, 330 University Avenue  
CITY: Toronto  
STATE: Ontario  
COUNTRY: Canada  
ZIP: MSG 1R7  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/452,531  
FILING DATE:  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/115,987  
FILING DATE: 03-SEP-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: STEWART, Michael I.  
REGISTRATION NUMBER: 24,973  
REFERENCE/DOCKET NUMBER: 1038-448 MIS:bh  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (416) 595-1155  
TELEFAX: (416) 595-1163  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 236 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-452-531-3

Query Match Score 73.5; DB 4; Length 447;  
Best Local Similarity 34.1%; Pred. No. 2.1;  
Matches 29; Conservative 9; Mismatches 26; Indels 21; Gaps 4;

Qy 35 ALESAAPAGATLNLPLK-----LISS-----IGIPVNHLIEGSQKCV 79  
Db 328 ALPEALEGS-----QSQPVEPDGPAGAVELCLVLSGMLVPELAIPVVYL-GALITML 381

Qy 80 AEIQPQAVGAVKALKALGALTVFG 104  
Db 382 SETRAQAGGGAGVAELGPBLELVG 406

RESULT 14  
US-09-523-849-34  
Sequence 34, Application US/09523849  
Patent No. 645561  
GENERAL INFORMATION:  
APPLICANT: Bandman, Olga  
APPLICANT: Molteni, Angela  
APPLICANT: Magnaghi, Paola  
APPLICANT: Bosotti, Roberta  
APPLICANT: Scacheri, Emanuela  
APPLICANT: Isacchi, Antonella  
APPLICANT: Hodson, Dave  
TITLE OF INVENTION: NIM1 KINASE  
FILE REFERENCE: PC-00009 US  
CURRENT APPLICATION NUMBER: US/09/523,849  
CURRENT FILING DATE: 2000-03-13  
NUMBER OF SEQ ID NOS: 39  
SOFTWARE: PERL Program  
SEQ ID NO: 34  
LENGTH: 776  
TYPE: PRT  
ORGANISM: Rattus norvegicus  
FEATURE:  
NAME/KEY: misc feature  
OTHER INFORMATION: GenBank Accession No. 6458561 g5672676  
US-09-523-849-34

Query Match Score 14.6%; DB 4; Length 776;  
Best Local Similarity 33.7%; Pred. No. 4.5%;  
Matches 28; Conservative 11; Mismatches 31; Indels 13; Gaps 4;

Qy 10 CVALSCKSAAAFLVGSQKCYAELGQA-VGA 89  
Db 490 CIVVSSAAVSSEGTSIDSCLFSASEGPAGLGG-LATGLGLTSVPLASPL--- 545

Qy 68 VNHLIESQSKCYAELGQA-VGA 89  
Db 546 -----GSQSATPVLQQAGLGA 562

Search completed: June 2, 2004, 20:23:17  
Job time : 8.24797 sec

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.	protein - protein search, using sw model	US-09-700-770-9	502	502	100.0	104	6	ADA17936
	Sequence:	1 MKLAALLGLCVALSQSSAAA.....QAVGAVKALKALLGGALTIVFG 104			502	100.0	104	6
on:	June 2, 2004, 19:59:24 ; Search time 24.778 Seconds (without alignments)	BLOSUM62			502	100.0	104	6
oring table:	Gapop 10.0 , Gapext 0.5	Gapop 10.0 , Gapext 0.5			502	100.0	104	6
arched:	1586107 seqs, 282547505 residues				502	100.0	104	7
total number of hits satisfying chosen parameters:	1586107				502	100.0	104	7
minimum DB seq length:	0				502	100.0	104	7
maximum DB seq length:	20000000000				502	100.0	104	7
rst-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries				502	100.0	104	7
atabase :	A_GenSeq_29Jan04:*				502	100.0	104	7
	1: GenSeqDP19908:*				502	100.0	104	7
	2: GenSeqDP20008:*				502	100.0	104	7
	3: GenSeqDP20018:*				502	100.0	104	7
	4: GenSeqDP20028:*				502	100.0	104	7
	5: GenSeqDP20038:*				502	100.0	104	7
	6: GenSeqDP20048:*				502	100.0	104	7
	7: GenSeqDP20058:*				502	100.0	104	7
	8: GenSeqDP20068:*				502	100.0	104	7
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.								
SUMMARIES								
Result No.	Score	Query Match	Length	DB ID	Description			
1	502	100.0	104	3 AAY66757	Aay66757 Membrane-lun	PR 02-JUN-1998;	98US-0087607P.	
2	502	100.0	104	3 AAY44458	Aay44458 Human lun	PR 02-JUN-1998;	98US-0087608P.	
3	502	100.0	104	3 AAY87288	Aay87288 Human sig	PR 03-JUN-1998;	98US-0087759P.	
4	502	100.0	104	4 AAB63280	Aab63280 Human PRO	PR 04-JUN-1998;	98US-0088021P.	
5	502	100.0	104	5 AAU86141	Aau86141 Human PRO	PR 04-JUN-1998;	98US-0088025P.	
6	502	100.0	104	6 ABU5895	Abu5895 Human PRO	PR 04-JUN-1998;	98US-0088028P.	
7	502	100.0	104	6 ABU59173	Abu59173 Novel hum	PR 04-JUN-1998;	98US-0088030P.	
8	502	100.0	104	6 ABU82685	Abu82685 Human PRO	PR 04-JUN-1998;	98US-0088033P.	
9	502	100.0	104	6 AAO19895	Aao19895 Human utte	PR 04-JUN-1998;	98US-0088326P.	
10	502	100.0	104	6 ABU60604	Abu60604 Human sec	PR 05-JUN-1998;	98US-0088167P.	
11	502	100.0	104	6 ABU13986	Abu13986 Human PRO	PR 05-JUN-1998;	98US-0088202P.	
12	502	100.0	104	6 ABU72571	Abu72571 Novel hum	PR 05-JUN-1998;	98US-0088212P.	
13	502	100.0	104	6 ABU59320	Abu59320 Human sec	PR 05-JUN-1998;	98US-0088217P.	
14	502	100.0	104	6 ABO26017	Abo26017 Human PRO	PR 10-JUN-1998;	98US-0088655P.	
15	502	100.0	104	6 ABU59026	Abu59026 Human sec	PR 10-JUN-1998;	98US-0088722P.	
16	502	100.0	104	6 ABU92404	Abu92404 Novel hum	PR 10-JUN-1998;	98US-0088730P.	
17	502	100.0	104	6 ABU59469	Abu59469 Novel hum	PR 10-JUN-1998;	98US-0088734P.	
18	502	100.0	104	6 ABU92235	Abu92235 Novel hum	PR 10-JUN-1998;	98US-0088738P.	
19	502	100.0	104	6 ABU10941	Abu10941 Human PRO	PR 10-JUN-1998;	98US-0088740P.	
20	502	100.0	104	6 ABU81693	Abu81693 Novel hum	PR 10-JUN-1998;	98US-0088741P.	
21	502	100.0	104	6 ABO88632	Abo88632 Human sec	PR 10-JUN-1998;	98US-0088742P.	
22	502	100.0	104	6 ABO34146	Abo34146 Human PRO	PR 10-JUN-1998;	98US-0088810P.	
23	502	100.0	104	6 ADA37919	Ada37919 Human sec	PR 10-JUN-1998;	98US-0088811P.	
24	502	100.0	104	6 ADA21605	Ada21605 Human sec	PR 10-JUN-1998;	98US-0088824P.	
25	502	100.0	104	6 ADA10392	Ada10392 Human sec	PR 10-JUN-1998;	98US-0088825P.	

PR 10-JUN-1998; 98US-00888826P.  
 PR 11-JUN-1998; 98US-00888858P.  
 PR 11-JUN-1998; 98US-00888861P.  
 PR 11-JUN-1998; 98US-00888863P.  
 PR 11-JUN-1998; 98US-00888876P.  
 PR 12-JUN-1998; 98US-00889090P.  
 PR 12-JUN-1998; 98US-00889105P.  
 PR 16-JUN-1998; 98US-008944P.  
 PR 16-JUN-1998; 98US-0089512P.  
 PR 16-JUN-1998; 98US-0089514P.  
 PR 17-JUN-1998; 98US-0089532P.  
 PR 18-JUN-1998; 98US-0089534P.  
 PR 17-JUN-1998; 98US-0089538P.  
 PR 17-JUN-1998; 98US-0089539P.  
 PR 17-JUN-1998; 98US-0089599P.  
 PR 19-JUN-1998; 98US-0089610P.  
 PR 17-JUN-1998; 98US-0089612P.  
 PR 19-JUN-1998; 98US-00896514P.  
 PR 22-JUN-1998; 98US-0089653P.  
 PR 22-JUN-1998; 98US-0090252P.  
 PR 22-JUN-1998; 98US-0090354P.  
 PR 23-JUN-1998; 98US-0090349P.  
 PR 23-JUN-1998; 98US-0090355P.  
 PR 24-JUN-1998; 98US-0090452P.  
 PR 24-JUN-1998; 98US-00904246P.  
 PR 24-JUN-1998; 98US-0090431P.  
 PR 24-JUN-1998; 98US-0090435P.  
 PR 24-JUN-1998; 98US-0090444P.  
 PR 24-JUN-1998; 98US-0090445P.  
 PR 24-JUN-1998; 98US-0090461P.  
 PR 24-JUN-1998; 98US-0090472P.  
 PR 24-JUN-1998; 98US-0090555P.  
 PR 24-JUN-1998; 98US-0090538P.  
 PR 24-JUN-1998; 98US-0090540P.  
 PR 24-JUN-1998; 98US-0090557P.  
 PR 25-JUN-1998; 98US-0090567P.  
 PR 25-JUN-1998; 98US-0090678P.  
 PR 25-JUN-1998; 98US-0090680P.  
 PR 25-JUN-1998; 98US-0090690P.  
 PR 25-JUN-1998; 98US-0090692P.  
 PR 25-JUN-1998; 98US-0090694P.  
 PR 02-JUL-1998; 98US-0091360P.  
 PR 02-JUL-1998; 98US-0091478P.  
 PR 02-JUL-1998; 98US-0091486P.  
 PR 02-JUL-1998; 98US-0091519P.  
 PR 02-JUL-1998; 98US-0091544P.  
 PR 02-JUL-1998; 98US-0091526P.  
 PR 02-JUL-1998; 98US-0091628P.  
 PR 02-JUL-1998; 98US-0091633P.  
 PR 02-JUL-1998; 98US-0091646P.  
 PR 02-JUL-1998; 98US-0091673P.  
 PR 07-JUL-1998; 98US-0091979P.  
 PR 07-JUL-1998; 98US-0091982P.  
 PR 09-JUL-1998; 98US-009182P.  
 PR 10-JUL-1998; 98US-0092472P.  
 PR 20-JUL-1998; 98US-0093339P.  
 PR 30-JUL-1998; 98US-0094651P.  
 PR 04-AUG-1998; 98US-009282P.  
 PR 04-AUG-1998; 98US-009285P.  
 PR 04-AUG-1998; 98US-009302P.  
 PR 04-AUG-1998; 98US-009318P.  
 PR 04-AUG-1998; 98US-0095121P.  
 PR 04-AUG-1998; 98US-0093325P.  
 PR 10-AUG-1998; 98US-0095916P.

98US-0095929P.  
 PR 10-AUG-1998; 98US-0096012P.  
 PR 11-AUG-1998; 98US-0096146P.  
 PR 11-AUG-1998; 98US-0096329P.  
 PR 12-AUG-1998; 98US-0096757P.  
 PR 17-AUG-1998; 98US-0096766P.  
 PR 17-AUG-1998; 98US-0096768P.  
 PR 17-AUG-1998; 98US-0096773P.  
 PR 17-AUG-1998; 98US-0096791P.  
 PR 17-AUG-1998; 98US-009687P.  
 PR 17-AUG-1998; 98US-0096891P.  
 PR 17-AUG-1998; 98US-0096894P.  
 PR 17-AUG-1998; 98US-0096895P.  
 PR 17-AUG-1998; 98US-0096910P.  
 PR 17-AUG-1998; 98US-0096947P.  
 PR 18-AUG-1998; 98US-0096949P.  
 PR 18-AUG-1998; 98US-0096950P.  
 PR 18-AUG-1998; 98US-0096959P.  
 PR 18-AUG-1998; 98US-0096960P.  
 PR 18-AUG-1998; 98US-0097022P.  
 PR 19-AUG-1998; 98US-0097141P.  
 PR 20-AUG-1998; 98US-0097218P.  
 PR 24-AUG-1998; 98US-0097611P.  
 PR 26-AUG-1998; 98US-0097951P.  
 PR 26-AUG-1998; 98US-0097952P.  
 PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097955P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097974P.  
 PR 26-AUG-1998; 98US-0097978P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 26-AUG-1998; 98US-0097986P.  
 PR 26-AUG-1998; 98US-0098014P.  
 PR 31-AUG-1998; 98US-0098325P.  
 PR 16-SEP-1998; 98US-010034P.  
 PR 12-JAN-1999; 99US-0115565P.  
 XX (GEIH ) GENENTECH INC.  
 XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX Claim 12; Fig 290; 822p; English.  
 XX WPI: 2000-072883/06.  
 DR N-PSDB; AA265103.  
 XX Membrane-bound proteins and related nucleotide sequences.  
 XX PT  
 XX CC  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC molecules are useful as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
 CC also be useful for the preparation of PRO polypeptides, especially by  
 CC recombinant techniques  
 XX Sequence 104 AA:  
 SQ Query Match Score 502; DB 3;  
 Best Local Similarity 100.0%; Pred. No. 1, 4e-48;  
 Match:B 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLALLGLCVALSCKSAAAFLGSAKPVQAOPVYALSAEAGTIANPLGTINPLKL 60  
 DB 1 MKLALLGLCVALSCKSAAAFLGSAKPVQAOPVYALSAEAGTIANPLGTINPLKL 60

RESULT 2  
 AAY44458  
 ID AAY44458 standard; protein: 104 AA.  
 XX  
 AC AAY44458;  
 XX  
 DT 27-MAR-2000 (first entry)  
 XX  
 DE Human lung specific gene protein Lng107.  
 XX  
 KW Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;  
 XX lung cancer; diagnosis.  
 XX Homo sapiens.  
 XX WO9960160-A1.  
 XX  
 PD 25-NOV-1999.  
 XX  
 PF 12-MAY-1999; 99WO-US010344.  
 XX  
 PR 21-MAY-1998; 98US-0086212P.  
 XX  
 PA (DIAD-) DIADEXUS LLC.  
 XX  
 PI Yang F, Macina RA, Sun Y;  
 XX  
 DR 2000-11-16320/10.  
 XX  
 DR N-PSDB; AAZ29723.  
 XX  
 PT A new method for diagnosing, monitoring and staging lung cancer.  
 XX  
 Example 2; Page 38-39; 40pp; English.  
 XX  
 The present sequence is a lung specific gene (LSG) protein Lng107 from  
 CC human clone ID 582271. The LSG has high level of tissue specificity for  
 CC lungs and is overexpressed in cancerous tissues. The sequence serves as a  
 CC diagnostic marker for detecting, monitoring, staging and prognosticating  
 CC lung cancer. The diagnosis involves comparing levels of LSG in samples  
 CC obtained from patient and normal control.  
 XX Sequence 104 AA;  
 XX  
 Query Match 100.0%; Score 502; DB 3; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.e-48;  
 Matches 104; Conservative 0; Mismatches 0; Gaps 0;  
 CC  
 CC 1 MKLAAILGLCVALSSCAAFLVGSAKPAQPVALESAAEAGGTLANPLGTINPLKLU 60  
 CC 1 MKLAAILGLCVALSSCAAFLVGSAKPAQPVALESAAEAGGTLANPLGTINPLKLU 60  
 CC  
 CC 61 LSSLGIPVNHLIEGSOKCVAEGLGPAVGAVKALKGALTIVFG 104  
 CC 61 LSSLGIPVNHLIEGSOKCVAEGLGPAQVGAVKALKGALTIVFG 104  
 CC  
 CC

RESULT 3  
 AAY87288  
 ID AAY87288 standard; protein: 104 AA.  
 XX  
 AC AAY87288;  
 XX  
 DT 11-MAY-2000 (first entry)  
 XX  
 DE Human signal peptide containing protein HSPP-65 SEQ ID NO:65.  
 XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;

KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;  
 KW antisthmatic; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arterioclecosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's disease; cvulatory defect;  
 KW muscular dystrophy.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200000610-A2.  
 XX  
 PD 06-JAN-2000.  
 XX  
 PF 25-JUN-1999; 99WO-US014484.  
 XX  
 PR 26-JUN-1998; 98US-0090762P.  
 PR 31-JUN-1998; 98US-0094983P.  
 PR 01-OCT-1998; 98US-0102886P.  
 PR 11-DEC-1998; 98US-0112429P.  
 XX  
 PA (INC(-)) INCYTE PHARM INC.  
 XX  
 PI Lal <sup>2</sup>, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
 PI Patterson C, Reddy R, Hillman JL;  
 PI Akerman IE,  
 PI Bandman O;  
 XX  
 DR WPI; 2000-160673/14.  
 DR N-PSDB; AAZ298173.  
 XX  
 PT New human signal peptide-containing proteins useful in treatment, prevention and diagnosis of e.g. cancer, inflammation and cardiovascular disease.  
 PT  
 XX  
 PS Claim 1; Page 205; 327pp; English.  
 XX  
 AAZ98109 to AAZ98242 encode AAY87224 to AAY87357 which represent the human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have anti-inflammatory, antimicrobial, nootropic, hepatotropic, antisthmatic, cardio-vascular, anti-asthmatic activities, and can be used in gene therapy. HSPPs can be used to treat or prevent disorders associated with decreased activity or function of HSPP. Antagonists of HSPP are used to treat or prevent disorders associated with increased activity or function of HSPP. Such diseases include cell proliferation (including cancer), inflammation, cardiovascular, neurological, reproductive or developmental disorders, (e.g. arteriosclerosis, cirrhosis, poriasis, acquired immune deficiency syndrome, anaemia, asthma, Crohn's disease, microbial or other infection, congestive or ischaemic heart disease, Alzheimer's or Huntington's disease, schizophrenia, ornulatory defects, muscular dystrophy). HSPP nucleic acids can be used for the recombinant production of HSPP, for detecting HSPP in standard hybridisation and amplification assays (for diagnosis and monitoring), in gene therapy, as antisense, triplex-forming or ribozyme therapeutics, for detecting related sequences or genetic variations, and for chromosomal mapping. HSPP are also used to raise specific antibodies (Ab) and to screen for agonists and antagonists (potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP -related diseases (in usual immunoassays), as therapeutic antagonists, in competitive drug screens, and for purification of HSPP from natural sources  
 XX  
 SQ Sequence 104 AA;  
 XX  
 Query Match 100.0%; Score 502; DB 3; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.e-48;  
 Matches 104; Conservative 0; Mismatches 0; Gaps 0;  
 CC  
 CC 1 MKLAAILGLCVALSSCAAFLVGSAKPAQPVALESAAEAGGTLANPLGTINPLKLU 60  
 CC 1 MKLAAILGLCVALSSCAAFLVGSAKPAQPVALESAAEAGGTLANPLGTINPLKLU 60  
 CC  
 CC 61 LSSLGIPVNHLIEGSOKCVAEGLGPAVGAVKALKGALTIVFG 104  
 CC 61 LSSLGIPVNHLIEGSOKCVAEGLGPAQVGAVKALKGALTIVFG 104  
 CC  
 CC

Query Match 100.0%; Score 502; DB 3; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.e-48;  
 Matches 104; Conservative 0; Mismatches 0; Gaps 0;  
 CC  
 CC 1 MKLAAILGLCVALSSCAAFLVGSAKPAQPVALESAAEAGGTLANPLGTINPLKLU 60  
 CC 1 MKLAAILGLCVALSSCAAFLVGSAKPAQPVALESAAEAGGTLANPLGTINPLKLU 60  
 CC  
 CC 61 LSSLGIPVNHLIEGSOKCVAEGLGPAVGAVKALKGALTIVFG 104  
 CC 61 LSSLGIPVNHLIEGSOKCVAEGLGPAQVGAVKALKGALTIVFG 104  
 CC  
 CC

chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO nucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF4470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF4087 to AAF44299 and AAB6154 to AAB6300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention	
XX Sequence 104 AA: SQ	Query Match 100.0%; Score 502; DB 4; Length 104; Best Local Similarity 100.0%; Pred. No. 1. 4e-48; Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Qy 1 MKAIAAFLGCVALSQSSAAFLYGSAKPVQAQPVVALESAAEAGACTLNLPLGTLNPPLKLL 60 Db 1 MKAIAAFLGCVALSQSSAAFLYGSAKPVQAQPVVALESAAEAGACTLNLPLGTLNPPLKLL 60	
XX	61 LSSIGIPTYNHLIGSOKCYAELGQAVGAVKALKLALLGALTIVFG 104
Qy 61 LSSIGIPTYNHLIGSOKCYAELGQAVGAVKALKLALLGALTIVFG 104 Db 61 LSSIGIPTYNHLIGSOKCYAELGQAVGAVKALKLALLGALTIVFG 104	
RESULT 5 AAU86141 ID AAU86141 Standard; protein; 104 AA. XX AAU86141; AC XX DT 15-JUL-2002 (first entry) XX DB Human PRO1245 polypeptide. XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy; leukaemia; neuronal disorder; stromal disorder; blastocellic disorder; inflammatory disorder; immune disorder; angiogenic disorder; cytostatic; neuro-protective. XX Homo sapiens. XX WO2010153486-A1. XX PN WO2010153486-A1. XX PD 26-JUL-2001. XX PF 11-FEBB-2000; 2000WO-US035655. XX PR 08-MAR-1999; 99WO-US05028. PR 11-MAR-1999; 99US-0123972P. PR 11-MAY-1999; 99US-0133459P. PR 02-JUN-1999; 99WO-US03252. PR 22-JUN-1999; 99US-0140650P. PR 22-JUN-1999; 99US-0140653P. PR 20-JUL-1999; 99US-014478P. PR 26-JUL-1999; 99US-014568P. PR 28-JUL-1999; 99US-014622P. PR 17-AUG-1999; 99US-014399P. PR 31-AUG-1999; 99US-015168P. PR 01-SEP-1999; 99WO-US020111. PR 15-SEP-1999; 99WO-US021090. PR 30-NOV-1999; 99WO-US028313. PR 01-DEC-1999; 99WO-US028301. PR 01-DEC-1999; 99WO-US028634. PR 05-JAN-2000; 2000WO-US000219. XX (GETH ) GENENTECH INC. XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillian KJ; PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM; PI Watanaabe CK, XX DR WO2002-205567/26.	

DR N-PSDB; ABK40267.  
 XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
 PT benign or malignant tumors, leukemias and lymphoid malignancies,  
 PT inflammatory, angiogenic and immunologic disorders.  
 XX

## Claim 61; Fig 28; 302pp; English.

XX The present invention relates to the isolation of novel human PRO polypeptides and the polynucleotide sequences encoding them. The PRO polypeptides, agonists, antagonists, antibodies are useful for treating benign or malignant tumours (e.g. renal, kidney, bladder, breast, etc), leukaemias and lymphoid malignancies, other disorders such as neuronal, glial, astrocytic, hypothalamic, glandular, macrophagal, stromal and blastocoelic disorders, inflammatory, immune and angiogenic disorders. The polynucleotide sequences are also useful in gene therapy. AAU86128-AAU86162 represent the human PRO polypeptides of the invention.

XX Sequence 104 AA;

Query Match 100.0%; Score 502; DB 5; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1 4e-48; Indels 0; Gaps 0;

Matches 104; Conservative 0; Mismatches 0;

CC 1 MKLALLGLGVALSSAAFLVGSAKPVQAQPVAALESAAEAGACTLAPLGTNPLKL 60  
 CC 1 MKLALLGLGVALSSAAFLVGSAKPVQAQPVAALESAAEAGACTLAPLGTNPLKL 60

Db 61 LSSLGIPVNHLLEGSQLKCVAELGPQAVGAVKALKALLGALTVEG 104

Db 61 LSSLGIPVNHLLEGSQLKCVAELGPQAVGAVKALKALLGALTVEG 104

## RESULT 6

ID ABUS8095 standard; protein; 104 AA.

XX ABUS8095;

XX DT 14-APR-2003 (first entry)

XX Human PRO polypeptide #127.

XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;

XX horse; cow; dog; cat; sheep; pig; goat; rabbit; ADPT;

XX antibody-dependent enzyme mediated prodrug therapy.

OS Homo sapiens.

PN US2003027163-A1.

XX PD 06-FEB-2003.

XX PP 15-NOV-2001; 2001US-00997666.

XX PR 16-JUN-1997; 97US-0049787P.

PR 17-OCT-1997; 97US-006220P.

PR 12-NOV-1997; 97WO-006518P.

PR 13-NOV-1997; 97US-005311P.

PR 24-NOV-1997; 97US-0066770P.

PR 25-FEB-1998; 98US-0075945P.

PR 20-MAR-1998; 98US-0077891QP.

PR 28-APR-1998; 98US-0083322P.

PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-008710P.

PR 02-JUN-1998; 98US-008760P.

PR 02-JUN-1998; 98US-008760P.

PR 02-JUN-1998; 98US-008775P.

PR 03-JUN-1998; 98US-008782P.

PR 04-JUN-1998; 98US-008802P.

PR 04-JUN

PR	04-AUG-1998;	98US-0095282P.	PR	02-MAR-2000;	2000WO-US005841.
PR	04-AUG-1998;	98US-0095285P.	PR	10-MAR-2000;	2000WO-US006319.
PR	04-AUG-1998;	98US-0095301P.	PR	15-MAR-2000;	2000WO-US006884.
PR	04-AUG-1998;	98US-0095302P.	PR	20-MAR-2000;	2000WO-US007377.
PR	04-AUG-1998;	98US-0095318P.	PR	30-MAR-2000;	2000WO-US008439.
PR	04-AUG-1998;	98US-0095321P.	PR	15-MAY-2000;	2000WO-US013358.
PR	04-AUG-1998;	98US-0095325P.	PR	17-MAY-2000;	2000WO-US013705.
PR	10-AUG-1998;	98US-0095316P.	PR	22-MAY-2000;	2000WO-US014042.
PR	10-AUG-1998;	98US-0095329P.	PR	30-MAY-2000;	2000WO-US014941.
PR	10-AUG-1998;	98US-0096102P.	PR	02-JUN-2000;	2000WO-US015264.
PR	11-AUG-1998;	98US-0096143P.	PR	23-JUN-2000;	2000WO-US0213637P.
PR	11-AUG-1998;	98US-0096144P.	PR	28-JUL-2000;	2000WO-US020710.
PR	12-AUG-1998;	98US-0096329P.	PR	11-AUG-2000;	2000WO-US022031.
PR	17-AUG-1998;	98US-0096757P.	PR	23-AUG-2000;	2000WO-US023522.
PR	17-AUG-1998;	98US-0096766P.	PR	24-AUG-2000;	2000WO-US023328.
PR	17-AUG-1998;	98US-0096773P.	PR	07-SEP-2000;	2000US-0230978P.
PR	17-AUG-1998;	98US-0096771P.	Query Match	.100.0%;	Score 502;
PR	17-AUG-1998;	98US-0096867P.	Best Local Similarity	100.0%;	DB 6;
PR	17-AUG-1998;	98US-0096871P.	No. 1.4e-48;	Length 104;	
PR	17-AUG-1998;	98US-0096891P.	Matches 0;	Mismatches 0;	
PR	17-AUG-1998;	98US-0096894P.	Indels 0;	Gaps 0;	
PR	17-AUG-1998;	98US-0096895P.			
PR	17-AUG-1998;	98US-0096897P.			
PR	18-AUG-1998;	98US-0096349P.			
PR	18-AUG-1998;	98US-009650P.			
PR	18-AUG-1998;	98US-009655P.			
PR	18-AUG-1998;	98US-0096959P.			
PR	18-AUG-1998;	98US-0096960P.			
PR	18-AUG-1998;	98US-0097022P.			
PR	19-AUG-1998;	98US-0097141P.			
PR	20-AUG-1998;	98US-0097218P.			
PR	24-AUG-1998;	98US-0097665P.			
PR	26-AUG-1998;	98US-0097954P.			
PR	26-AUG-1998;	98US-0097955P.			
PR	26-AUG-1998;	98US-0097971P.			
PR	26-AUG-1998;	98US-0097974P.			
PR	26-AUG-1998;	98US-0097978P.			
PR	26-AUG-1998;	98US-0097979P.			
PR	26-AUG-1998;	98US-0097986P.			
PR	26-AUG-1998;	98US-0098014P.			
PR	16-SEP-1998;	98US-0098529P.			
PR	16-SEP-1998;	98US-0100634P.			
PR	16-SEP-1998;	98WO-US019330.			
PR	17-SEP-1998;	98US-0100855P.			
PR	17-SEP-1998;	98WO-US019437.			
PR	07-OCT-1998;	98WO-US021141.			
PR	01-DEC-1998;	98WO-US025108.			
PR	22-DEC-1998;	98US-011329P.			
PR	05-JAN-1999;	99WO-US000106.			
PR	08-MAR-1999;	99WO-US005028.			
PR	12-MAR-1999;	99US-0123957P.			
PR	02-JUN-1999;	99WO-US012252.			
PR	23-JUN-1999;	99US-0141037P.			
PR	07-JUL-1999;	99US-0143048P.			
PR	20-JUL-1999;	99US-0144759P.			
PR	28-JUL-1999;	99US-0145698P.			
PR	17-AUG-1999;	99US-0146222P.			
PR	15-SEP-1999;	99US-0149396P.			
PR	15-SEP-1999;	99WO-US02190.			
PR	15-SEP-1999;	99WO-US01547.			
PR	08-OCT-1999;	99US-018663P.			
PR	30-NOV-1999;	99WO-US028313.			
PR	01-DEC-1999;	99WO-US028301.			
PR	01-DEC-1999;	99WO-US028634.			
PR	16-DEC-1999;	99WO-US031095.			
PR	20-DEC-1999;	99WO-US031911.			
PR	05-JAN-2000;	2000WO-US000219.			
PR	06-JAN-2000;	2000WO-US00376.			
PR	11-FEB-2000;	2000WO-US003565.			
PR	18-FEB-2000;	2000WO-US004341.			
PR	22-FEB-2000;	2000WO-US004414.			
PR	24-FEB-2000;	2000WO-US004914.			
PR	24-FEB-2000;	2000WO-US005004.			
		2000WO-US005004.			
		2000US-0230978P.			
		98US-0087759P.			

Query Match .100.0%; Score 502; DB 6; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
 Matches 104; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

RESULT 7  
 ABU59173 standard; protein; 104 AA.  
 ID ABU59173;  
 AC ABU59173;  
 XX ABU59173;  
 XX 28-APR-2003 (first entry)

Novel human secreted or transmembrane protein PRO1245.  
 DE Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;  
 Human; cardiac insufficiency disorder; cancer; tumour; immune response;  
 Human; adrenal cortical capillary endothelial growth; c-fos induction;  
 Human; vascular endothelial growth factor inhibition; VEGF inhibition;  
 Human; endothelial cell growth inhibitor; T-lymphocytes stimulation;  
 Human; retinal neurons cell survival; rod photoreceptor cell survival;  
 Human; retinal disorders; retinipax pigmentosum; kidney disorder;  
 Human; mammalian kidney megalangi cell proliferation; Berger disease;  
 Human; dermatis; herpetiformis; Crohn's disease; chondrocyte proliferation;  
 Human; chondrocyte redifferentiation; sports injury; arthritis;  
 Homo sapiens.

XX OS US2002132252-A1.  
 PN US2002132252-A1.  
 XX PD 19-SEP-2002.  
 XX PR 14-NOV-2001; 2001US-00990442.  
 XX PR 16-JUN-1997; 97US-0049787P.  
 PR 17-JUL-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020063.  
 PR 12-NOV-1997; 97US-0065186P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 24-NOV-1997; 97US-0066710P.  
 PR 25-FEB-1998; 98US-0075941P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
 PR 07-MAY-1998; 98US-0084600P.  
 PR 28-MAY-1998; 98US-0087106P.  
 PR 02-JUN-1998; 98US-0087607P.  
 PR 02-JUN-1998; 98US-0087609P.  
 PR 02-JUN-1998; 98US-0087759P.

PR 03-JUN-1998; 98US-0087827P.  
 PR 04-JUN-1998; 98US-0088021P.  
 PR 04-JUN-1998; 98US-0088025P.  
 PR 04-JUN-1998; 98US-0088026P.  
 PR 04-JUN-1998; 98US-0088028P.  
 PR 04-JUN-1998; 98US-0088029P.  
 PR 04-JUN-1998; 98US-0088030P.  
 PR 04-JUN-1998; 98US-0088033P.  
 PR 04-JUN-1998; 98US-008826P.  
 PR 05-JUN-1998; 98US-0088167P.  
 PR 05-JUN-1998; 98US-0088202P.  
 PR 05-JUN-1998; 98US-008812P.  
 PR 05-JUN-1998; 98US-0088217P.  
 PR 09-JUN-1998; 98US-0088655P.  
 PR 10-JUN-1998; 98US-0088734P.  
 PR 10-JUN-1998; 98US-0088742P.  
 PR 10-JUN-1998; 98US-0088810P.  
 PR 10-JUN-1998; 98US-0088824P.  
 PR 10-JUN-1998; 98US-0088217P.  
 PR 11-JUN-1998; 98US-0088826P.  
 PR 11-JUN-1998; 98US-0088858P.  
 PR 11-JUN-1998; 98US-0088873P.  
 PR 12-JUN-1998; 98US-0088910P.  
 PR 16-JUN-1998; 98US-0088914P.  
 PR 16-JUN-1998; 98US-0088912P.  
 PR 16-JUN-1998; 98US-0088914P.  
 PR 17-JUN-1998; 98US-0088953P.  
 PR 17-JUN-1998; 98US-00889538P.  
 PR 17-JUN-1998; 98US-00889598P.  
 PR 17-JUN-1998; 98US-00889599P.  
 PR 17-JUN-1998; 98US-0088960P.  
 PR 17-JUN-1998; 98US-00889653P.  
 PR 18-JUN-1998; 98US-0089801P.  
 PR 18-JUN-1998; 98US-0089807P.  
 PR 18-JUN-1998; 98US-0089808P.  
 PR 16-SEP-1998; 98WO-US01933P.  
 PR 17-SEP-1998; 98WO-US01943P.  
 PR 07-OCT-1998; 98WO-US02114P.  
 PR 01-DEC-1998; 98WO-US02510P.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US11252.  
 PR 15-SEP-1999; 99WO-US02109P.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028534.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US03091P.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US004414.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006844.  
 PR 20-MAR-2000; 2000WO-US007237.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013338.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014931.  
 PR 02-JUN-2000; 2000WO-US01524.  
 PR 28-JUL-2000; 2000WO-US020701.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-NOV-2000; 2000WO-US030952.  
 PR 01-DEC-2000; 2000WO-US032678.

PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019632.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941932.  
 XX (GENTECH INC.  
 PA  
 XX  
 DR WPI: 2003-247083/24.  
 N-PSDB; ABX81385.  
 XX  
 PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Godowski PJ;  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Paoni NF;  
 PI Grimaldi JC, Gurney AL, Kljavin IU, Napier MA, Pan J,  
 Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX  
 PS Claim 12; Fig 290; 648PP; English.  
 XX  
 PT Novel isolated PRO polypeptides e.g. PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer treatments.  
 PT  
 XX  
 CC The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO1112 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536, PRO43, PRO826, PRO826, PRO1068 or PRO1355, PRO1126, PRO360 and PRO1387 induce c-fos in endothelial cells, and are thus useful for treating conditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonists of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular endothelial growth factor (VEGF) stimulated proliferation of endothelial cells and is thus useful for inhibiting endothelial cell growth in mammals which would be beneficial in inhibiting tumour growth. PRO826, PRO1184, PRO1346 and PRO1375 stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO1068 or PRO132 enhance survival of retinal neurons cells (PRO1132 is also enhances survival/proliferation of rod photoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosa, AMD, PRO819, PRO813 and PRO1106 induce proliferation of mammalian kidney mesangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function such as Berger disease or other nephropathies associated with dermatitis, herpetiformis or Crohn's disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the proliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein.  
 XX  
 SQ Sequence 104 AA;

Query	Match	100.0%	Score 502;	DB 6;	Length 104;
	Best Local Similarity	100.0%	Pred. No. 1.	4e-48;	
	Mismatches	0;	Conservative	0;	Gaps 0;
Qy	1 MKLAAIGLGLYALSCSSAAAFVGSAKPVAAQVALESAAFAAGATGLTANPLGTLNPFLKL 60				
Db	1 MKLAAIGLGLYALSCSSAAAVLGSAKPVAAQVALESAAFAAGATGLTANPLGTLNPFLKL 60				
Qy	61 LSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKGALTIVFG 104				
Db	61 LSSLGIPVNHLIEGSOKCVAELGPQAVGAVKALKGALTIVFG 104				

RESULT 8  
 ID ABU82685 standard; protein; 104 AA.

Page 8

XX	ABU82685;			98US-0089948P.
AC				98US-0089952P.
XX				98US-0090244P.
DDT				98US-0090252P.
XX				98US-0090348P.
DE	Human secreted/transmembrane protein PRO1245.			98US-0090355P.
XX				98US-0090429P.
KW	Human; PRO; secreted protein; transmembrane protein; angiogenesis; wound healing;			98US-0090431P.
KW	cardiac insufficiency disorders; immune response; retinal disorder; sight loss;			98US-0090433P.
KW	cancerous tumour; immune response; retinal disorder; sight loss;			98US-0090444P.
KW	retinitis pigmentosa; age-related macular degeneration; AMD;			98US-0090445P.
KW	kidney disorder; Berger disease; nephropathy; dermatitis; herpetiformis;			98US-0090474P.
KW	Crohn's disease; sports injury; arthritis;			98US-0090533P.
XX				98US-0090540P.
OS	Homo sapiens.			98US-0090542P.
XX				98US-0090557P.
PN	US2003032023-A1.			98US-0090676P.
XX				98US-0090678P.
PD	13-FEB-2003.			98US-0090690D.
XX				98US-0090694P.
PF	14-NOV-2001; 2001US-00990711.			98US-0090695P.
XX				98US-0090696P.
PR	16-JUN-1997;	97US-0049787P.		98US-0090697P.
PR	17-OCT-1997;	97US-006250P.		98US-0090698P.
PR	05-NOV-1997;	97WO-US020069.		98US-0090699P.
PR	12-NOV-1997;	97US-0065186P.		98US-0091360P.
PR	13-NOV-1997;	97US-0065311P.		98US-0091544P.
PR	24-NOV-1997;	97US-0166710P.		98US-0091478P.
PR	25-MAR-1998;	98US-0075454P.		98US-0091519P.
PR	20-MAR-1998;	98US-0078910P.		98US-0091626P.
PR	28-APR-1998;	98US-0108312P.		98US-0091628P.
PR	07-MAY-1998;	98US-0084500P.		98US-0091633P.
PR	28-MAY-1998;	98US-0087106P.		98US-0091646P.
PR	02-JUN-1998;	98US-0108760P.		98US-0091673P.
PR	02-JUN-1998;	98US-0087609P.		98US-0091978P.
PR	02-JUN-1998;	98US-0087759P.		98US-0091982P.
PR	03-JUN-1998;	98US-0108782P.		98US-0092118P.
PR	04-JUN-1998;	98US-0088021P.		98US-0092472P.
PR	04-JUN-1998;	98US-0088025P.		98US-0093339P.
PR	04-JUN-1998;	98US-0088026P.		98US-0094651P.
PR	04-JUN-1998;	98US-0088028P.		98US-0095282P.
PR	04-JUN-1998;	98US-0088039P.		98US-0095285P.
PR	04-JUN-1998;	98US-0088040P.		98US-0095301P.
PR	09-JUN-1998;	98US-0088031P.		98US-0095302P.
PR	04-JUN-1998;	98US-0088032P.		98US-0095318P.
PR	05-JUN-1998;	98US-0088167P.		98US-0095321P.
PR	05-JUN-1998;	98US-0088202P.		98US-0095325P.
PR	05-JUN-1998;	98US-0088212P.		98US-0095329P.
PR	05-JUN-1998;	98US-0088217P.		98US-0095929P.
PR	10-JUN-1998;	98US-0088265P.		98US-0096121P.
PR	10-JUN-1998;	98US-008855P.		98US-0096143P.
PR	11-JUN-1998;	98US-0088734P.		98US-0096146P.
PR	11-JUN-1998;	98US-0088738P.		98US-0096167P.
PR	11-JUN-1998;	98US-0088744P.		98US-0096757P.
PR	12-JUN-1998;	98US-0088810P.		98US-0096894P.
PR	10-JUN-1998;	98US-0088821P.		98US-0096895P.
PR	10-JUN-1998;	98US-0088826P.		98US-0096897P.
PR	11-JUN-1998;	98US-0088850P.		98US-0096791P.
PR	17-JUN-1998;	98US-0088861P.		98US-0096867P.
PR	17-JUN-1998;	98US-0088876P.		98US-0096867P.
PR	17-JUN-1998;	98US-0088910P.		98US-0096891P.
PR	16-JUN-1998;	98US-0089440P.		98US-0096892P.
PR	16-JUN-1998;	98US-0089512P.		98US-0097141P.
PR	16-JUN-1998;	98US-0089514P.		98US-0097218P.
PR	17-JUN-1998;	98US-0089532P.		98US-0097218P.
PR	18-JUN-1998;	98US-0089801P.		98US-0097218P.
PR	18-JUN-1998;	98US-0089907P.		98US-0097218P.
PR	18-JUN-1998;	98US-0089908P.		98US-0097218P.
PR	19-JUN-1998;	98US-0089947P.		98US-0097218P.
PR	19-JUN-1998;	98US-0089948P.		98US-0097218P.

PR	26-AUG-1998;	98US-0097955B.	DT	11-AUG-2003	(first entry)
PR	26-AUG-1998;	98US-0097971P.	XX	XX	Human uteroglobin related protein 2.
PR	26-AUG-1998;	98US-0097974P.	DE	XX	
PR	26-AUG-1998;	98US-0097978P.	XX	XX	UGRP1; human; mouse; promoter; uteroglobin related protein 1;
PR	26-AUG-1998;	98US-0097979P.	KW	XX	respiratory disorder; asthma.
PR	26-AUG-1998;	98US-0097986P.	KW	XX	
PR	26-AUG-1998;	98US-0098014P.	OS	XX	Homo sapiens.
PR	31-AUG-1998;	98US-0098525B.	XX	XX	
PR	16-SEP-1998;	98US-0100634P.	PN	PN	WO2003000111-A2.
PR	16-SEP-1998;	98US-01019330.	XX	XX	
PR	17-SEP-1998;	98US-0100858P.	PD	PD	03-JAN-2003.
PR	17-SEP-1998;	98US-0119437.	XX	XX	
PR	07-OCT-1998;	98US-010211141.	PF	PF	18-JUN-2002; 2002WO-US019456.
PR	01-DEC-1998;	98US-0125108.	XX	XX	
PR	22-DEC-1998;	98US-0113296P.	PR	PR	20-JUN-2001; 2001US-0299828P.
PR	05-JAN-1999;	99WO-US000106.	XX	XX	
PR	08-MAR-1999;	99WO-US005028.	PA	PA	(USSH ) US DEPT HEALTH & HUMAN SERVICES.
PR	12-MAR-1999;	99US-0123957P.	XX	XX	
PR	02-TUN-1999;	99WO-US012252.	PI	PI	Kimura S, Niimi T;
PR	02-TUN-1999;	99US-0141037P.	XX	XX	
PR	07-JUL-1999;	99US-0143048P.	DR	DR	WPI, 2003-184004/18.
PR	20-JUL-1999;	99US-0144758P.	PS	PS	Disclosure; Page 79-80; 83pp; English.
PR	26-JUL-1999;	99US-0145698P.	XX	XX	
PR	28-JUL-1999;	99US-0146222P.	PT	PT	New human UGRP1 nucleic acid, useful for diagnosing or predicting a predisposition to develop a respiratory disorder or determining the prognosis of a subject having or suspected of having a respiratory disorder e.g., asthma.
PR	17-AUG-1999;	99US-0143962P.	CC	CC	The present invention provides the human and murine uteroglobin related protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis of and prediction of predisposition to respiratory disorders such as CC
PR	15-SEP-1999;	99WO-US021090.	CC	CC	asthma. The present sequence is a protein sequence shown in the invention exemplification of the invention
PR	15-SEP-1999;	99WO-US02154.	CC	CC	
PR	08-OCT-1999;	99US-014863P.	XX	XX	
PR	30-NOV-1999;	99WO-US028313.	PS	PS	Sequence 104 AA;
PR	01-DEC-1999;	99WO-US028301.	XX	XX	Query Match Score 502; DB 6; Length 104;
PR	01-DEC-1999;	99WO-US028634.	PT	PT	Best Local Similarity 100.0%; Pred. No. 1.e-48;
PR	16-DEC-1999;	99WO-US03095.	CC	CC	Matches: 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
PR	20-DEC-1999;	99WO-US03091.	CC	CC	Qy 1 MKLAALLGLCVALCSSSAAFLVGSAKPVQAQPVALESAAAGACTLANPLGTINPLKLL 60
PR	05-JAN-2000;	99WO-US000219.	Db	Db	Db 1 MKLAALLGLCVALCSSSAAFLVGSAKPVQAQPVALESAAAGACTLANPLGTINPLKLL 60
PR	06-JAN-2000;	2000WO-US000376.	Qy	Qy	61 LSSLGIPVNHLIEGSQKCVAEGLGPOAVGAYKALKALKGALTIVFG 104
PR	11-FEB-2000;	2000WO-US003565.	Db	Db	Db 61 LSSLGIPVNHLIEGSQKCVAEGLGPOAVGAVKALKALKGALTIVFG 104
PR	18-FEB-2000;	2000WO-US00434.	RESULT 1)	RESULT 1)	RESULT 1)
PR	22-FEB-2000;	2000WO-US004414.	ABU6004	ABU6004	ABU6004
PR	24-FEB-2000;	2000WO-US004914.	ID	ID	ID ABU50604 standard; protein; 104 AA.
PR	02-MAR-2000;	2000WO-US00504.	XX	XX	
PR	10-MAR-2000;	2000WO-US00541.	AC	AC	
PR	15-MAR-2000;	2000WO-US006319.	XX	XX	
PR	20-MAR-2000;	2000WO-US00684.	DT	DT	01-MAY-2003 (first entry)
PR	30-MAR-2000;	2000WO-US008439.	XX	XX	
PR	15-MAY-2000;	2000WO-US01339.	DE	DE	Human secreted/transmembrane protein, #163.
PR	22-MAY-2000;	2000WO-US013105.	XX	XX	
PR	30-MAY-2000;	2000WO-US014042.	KW	KW	Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; therapeutic; gene therapy.
PR	02-JUN-2000;	2000WO-US01491.	OS	OS	Homo sapiens.
PR	23-JUN-2000;	2000WO-US021364.	XX	XX	
PR	28-JUL-2000;	2000WO-US020710.	PN	PN	US2002160384-A1.
PR	11-AUG-2000;	2000WO-US022303.	XX	XX	31-OCT-2002.
Qy	Matches 104; Conservative 0;	Score 502; DB 6; Length 104;	XX	XX	
Db	1 MKLAALLGLCVALCSSSAAFLVGSAKPVQAQPVALESAAAGACTLANPLGTINPLKLL 60	Best Local Similarity 100.0%; Pred. No. 1.e-48;	AC	AC	
Db	1 MKLAALLGLCVALCSSSAAFLVGSAKPVQAQPVALESAAAGACTLANPLGTINPLKLL 60	Mismatches 0; Indels 0; Gaps 0;	XX	XX	
Qy	61 LSSLGIPVNHLIEGSQKCVAEGLGPOAVGAVKALKALKGALTIVFG 104	Qy 1 MKLAALLGLCVALCSSSAAFLVGSAKPVQAQPVALESAAAGACTLANPLGTINPLKLL 60	XX	XX	
Db	61 LSSLGIPVNHLIEGSQKCVAEGLGPOAVGAVKALKALKGALTIVFG 104	Db 61 LSSLGIPVNHLIEGSQKCVAEGLGPOAVGAVKALKALKGALTIVFG 104	XX	XX	
RESULT 9	AA019895	RESULT 9	XX	XX	
ID	AA019895	ID AA019895 standard; protein; 104 AA.	PR	PR	14-NOV-2001; 2001US-00992598.
XX	AA019895;	XX	XX	16-JUN-1997; 97US-0049787P.	
XX	AA019895;	XX	XX		





CC from the USPTO web site at [seqdata.uspto.gov/pstplDIDEntry.html](http://seqdata.uspto.gov/pstplDIDEntry.html)

XX Sequence 104 AA;

Query Match 100.0%; Score 502; DB 6; Length 104;

Best Local Similarity 100.0%; Pred. No. 1.4e-48;

Mismatches 0; Conservative 0; Indels 0; Gaps 0;

Matches 104; Matches 104;

Qy 1 MKAALIGLCTALSCSAAAFYGSAXPVAQPVALESAAAGAGTANPLGTNPLKLL 60

Db 1 MKAALIGLCTALSCSAAAFYGSAXPVAQPVALESAAAGAGTANPLGTNPLKLL 60

Qy 61 LSSLGTPVNHJLEGSQKCVRAELGPOAYGVAKALKALLGALTIVFG 104

Db 61 LSSLGTPVNHJLEGSQKCVRAELGPOAYGVAKALKALLGALTIVFG 104

---

RESULT 12

ID ABU72571 standard; protein; 104 AA.

XX ABU72571;

XX 17-JUN-2003 (first entry)

XX Novel human secreted and transmembrane protein PRO1245.

DE Human secreted and transmembrane protein; cytostatic; anti-HIV; viricide; hepatotropic; antinflammatory; neuroprotective; gene therapy; PRO; pharmaceutical; diagnostic; biosensor; bioreactor; malignancy; cancer; ovarian cancer; colorectal cancer; Kapoor's sarcoma; leukaemia; lymphoma; hepatitis B; multiple sclerosis; Crohn's disease; RW drug screening.

XX Homo sapiens.

OS XX

PN US2003003531-A1.

XX PD 02-JAN-2003.

XX 19-NOV-2001; 2001US-00989734.

PF XX

PR 16-JUN-1997; 97US-0043787P.

PR 05-NOV-1997; 97US-0062250P.

PR 12-NOV-1997; 97WO-US2000069.

PR 13-NOV-1997; 97US-0065311P.

PR 24-NOV-1997; 97US-0065770P.

PR 25-FEB-1998; 98US-0075145P.

PR 20-MAR-1998; 98US-0078910P.

PR 28-APR-1998; 98US-0083122P.

PR 07-MAY-1998; 98US-0084600P.

PR 02-JUN-1998; 98US-0087160P.

PR 02-JUN-1998; 98US-0087607P.

PR 02-JUN-1998; 98US-0087690P.

PR 03-JUN-1998; 98US-0087754P.

PR 03-JUN-1998; 98US-0087759P.

PR 04-JUN-1998; 98US-0088030P.

PR 04-JUN-1998; 98US-0088032P.

PR 04-JUN-1998; 98US-0088033P.

PR 04-JUN-1998; 98US-0088360P.

PR 05-JUN-1998; 98US-0088167P.

PR 05-JUN-1998; 98US-0088220P.

PR 05-JUN-1998; 98US-0088224P.

PR 09-JUN-1998; 98US-0088655P.

PR 10-JUN-1998; 98US-0088734P.

PR 10-JUN-1998; 98US-0088738P.

PR 10-JUN-1998; 98US-0088742P.

PR 10-JUN-1998; 98US-0088810P.

PR 10-JUN-1998; 98US-0088824P.

PR 11-JUN-1998; 98US-0088826P.

PR 11-JUN-1998; 98US-0088858P.

PR 11-JUN-1998; 98US-0088861P.

PR 11-JUN-1998; 98US-0088876P.

PR 12-JUN-1998; 98US-0088105P.

PR 16-JUN-1998; 98US-0088440P.

PR 16-JUN-1998; 98US-0088512P.

PR 16-JUN-1998; 98US-0088514P.

PR 17-JUN-1998; 98US-0088932P.

PR 17-JUN-1998; 98US-0088938P.

PR 17-JUN-1998; 98US-0088958P.

PR 17-JUN-1998; 98US-0088959P.

PR 17-JUN-1998; 98US-0088960P.

PR 17-JUN-1998; 98US-0088953P.

PR 18-JUN-1998; 98US-0088901P.

PR 18-JUN-1998; 98US-0088907P.

PR 18-JUN-1998; 98US-0088908P.

PR 18-JUN-1998; 98WO-US019430.

PR 17-SEP-1998; 98WO-US021141.

PR 01-DEC-1998; 98WO-US025108.

PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US005028.

PR 12-JUN-1999; 99WO-US012552.

PR 17-SEP-1999; 99WO-US021090.

PR 07-JCT-1999; 99WO-US021547.

PR 01-FEB-2000; 2000WO-US00376.

PR 05-JAN-1999; 99WO-US028313.

PR 01-DEC-1999; 99WO-US028301.

PR 01-DEC-1999; 99WO-US02834.

PR 16-DEC-1999; 99WO-US030095.

PR 20-DEC-1999; 99WO-US030911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US004341.

PR 22-FEB-2000; 2000WO-US004414.

PR 24-FEB-2000; 2000WO-US004914.

PR 24-FEB-2000; 2000WO-US005004.

PR 02-MAR-2000; 2000WO-US05841.

PR 10-MAR-2000; 2000WO-US06319.

PR 15-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

PR 30-MAR-2000; 2000WO-US08439.

PR 15-MAY-2000; 2000WO-US13358.

PR 17-MAY-2000; 2000WO-US13705.

PR 22-MAY-2000; 2000WO-US14042.

PR 30-MAY-2000; 2000WO-US14941.

PR 02-JUN-2000; 2000WO-US15264.

PR 28-JUL-2000; 2000WO-US00520.

PR 11-AUG-2000; 2000WO-US022031.

PR 23-AUG-2000; 2000WO-US023522.

PR 24-AUG-2000; 2000WO-US023328.

PR 08-NOV-2000; 2000WO-US030952.

PR 01-DEC-2000; 2000WO-US32678.

PR 28-FEB-2001; 2001WO-US006520.

PR 01-JUN-2001; 2001WO-US017800.

PR 20-JUN-2001; 2001WO-US019692.

PR 29-JUN-2001; 2001WO-US021066.

PR 09-JUL-2001; 2001WO-US021735.

PR 28-AUG-2001; 2001US-00941992.

XX (GETH ) GENENTECH INC.

PA XX

PI Asbkenazi AJ, Baker KP, Borstein D, Deboyers L, Eaton DL, Goddowski PJ, Ferrara N, Fong S, Gerber R, Gerritsen ME, Goddowski A, Grimaldi JC, Gurney AL, Klagszn J, Napier MA, Pan J, Pachl NF, Roy MA, Stewart TA, Watanabe CK, Williams PM, Zhang Z;

PI DR WFI; 2003-352829/33.

DR N-PSDB; ACRA64431.

X New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's disease.

Claim 12: FIG 220; 663pp; English.

The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 203135, etc); or a sequence with at least 80% identity to a DNA encoding a PRO polypeptide. The PRO polypeptides or nucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These are particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, kaposi's sarcoma, or leukaemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's disease in mammals. The PRO polypeptides are useful in drug screening, particularly as targets for therapeutic intervention in these diseases, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel human secreted and transmembrane PRO polypeptide

Sequence 104 AA:						
	Query Match	Score	DB	Length	Indels	Gaps
Q	Best Local Similarity	100.0%	502;	6;	104;	0;
Q	Matches 104;	100.0%;	Pred. No.	1..4e-48;	Mismatches	0;
Q	Conservative	0;				
1	MKIAALIGCVALSCSSA	AFLVGSKPYAQPVAALESAA	ERAGGIFTANPDTGLTNP	LKLL	60	
1	MKIAALIGCVALSCSSA	AFLVGSKPYAQPVAALESAA	ERAGGIFTANPDTGLTNP	LKLL	60	
61	LSISIGIPVNHLIESQQ	KCYAELGPQAVGAVKALK	AIKGALGTVFG	104		
61	LSISIGIPVNHLIESQQ	KCYAELGPQAVGAVKALK	AIKGALGTVFG	104		

RESULT 13

KA	Homo sapiens.	
DS		24-JUN-1998; 98US-009054DP.
XX		PR 24-JUN-1998;
PN	US2003027162-A1.	PR 24-JUN-1998; 98US-009055TP.
XX		PR 25-JUN-1998; 98US-0090678P.
PD	06-FEB-2003.	PR 25-JUN-1998; 98US-0090678P.
XX		PR 25-JUN-1998; 98US-0090690P.
PF	15-NOV-2001; 2001US-00997428.	PR 25-JUN-1998; 98US-0090694P.
XX		PR 25-JUN-1998; 98US-0090695P.
PR	16-OCT-1997; 97US-0049787P.	PR 25-JUN-1998; 98US-0090695P.
PR	17-OCT-1997; 97US-002250P.	PR 26-JUN-1998; 98US-0090862P.
PR	17-OCT-1997; 97US-002250P.	PR 26-JUN-1998; 98US-0090863P.
PR	05-NOV-1997; 97NO-US020069.	PR 01-JUL-1998; 98US-0091136Q.
PR	12-NOV-1997; 97US-005186P.	PR 01-JUL-1998; 98US-0091154P.
PR	13-NOV-1997; 97US-005311P.	PR 02-JUL-1998; 98US-00911478P.
PR	24-NOV-1997; 97US-006770P.	PR 02-JUL-1998; 98US-0091519P.
PR	25-FEB-1998; 98US-0075945P.	PR 02-JUL-1998; 98US-0091626P.
PR	20-MAR-1998; 98US-0099910P.	PR 02-JUL-1998; 98US-0091626P.

PR 02-JUL-1998; 98US-0091628P.  
 PR 02-JUL-1998; 98US-0091633P.  
 PR 02-JUL-1998; 98US-0091646P.  
 PR 02-JUL-1998; 98US-0091673P.  
 PR 07-JUL-1998; 98US-0091978P.  
 PR 07-JUL-1998; 98US-0091982P.  
 PR 09-JUL-1998; 98US-0092122P.  
 PR 10-JUL-1998; 98US-0092427P.  
 PR 10-JUL-1998; 98US-0093339P.  
 PR 30-JUL-1998; 98US-0094511P.  
 PR 04-AUG-1998; 98US-0095282P.  
 PR 04-AUG-1998; 98US-0095285P.  
 PR 04-AUG-1998; 98US-0095302P.  
 PR 04-AUG-1998; 98US-0095312P.  
 PR 04-AUG-1998; 98US-0095318P.  
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 PR 26-AUG-1998; 98US-0097986P.  
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 PR 16-SEP-1998; 98US-0100634P.  
 PR 05-OCT-1998; 98WO-US019330.  
 PR 08-MAR-1999; 98WO-US005028.  
 PR 12-MAR-1999; 98WO-US0123957P.  
 PR 02-JUN-1999; 98WO-US012152.  
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 PR 01-DEC-1998; 98WO-US025108.  
 PR 22-DEC-1998; 98US-0113296P.  
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 PR 08-MAR-1999; 98WO-US005028.  
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 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.

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 PR 16-DEC-1999; 99WO-US010095.  
 PR 20-DEC-1999; 99WO-US010911.  
 PR 05-JAN-2000; 2000WO-US00219.  
 PR 06-JAN-2000; 2000WO-US00376.  
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 PR 22-FEB-2000; 2000WO-US04414.  
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 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
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 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US13358.  
 PR 17-MAY-2000; 2000WO-US13705.  
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 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 23-JUN-2000; 2000WO-US213637P.  
 PR 28-JUL-2000; 2000WO-US020710.  
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 PR 24-AUG-2000; 2000WO-US023328.

Query Match Score 502; DB 6; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
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Qy 1 MKLAALIGLYCALSSAAAFLVGSAKPVAAQVALESAAGAGTLANPLGTLAPLKL 60  
 Db 1 MKLAALIGLYCALSSAAAFLVGSAKPVAAQVALESAAGAGTLANPLGTLAPLKL 60

Query Match Score 502; DB 6; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 61 LSSGLIPVNHLLEGSQLKCVAAELGPQAVGAVKALKALGALTIVFG 104  
 Db 61 LSSGLIPVNHLLEGSQLKCVAAELGPQAVGAVKALKALGALTIVFG 104

RESULT 14  
 ABC26017 standard; protein; 104 AA.  
 XX  
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 AC ABC26017;  
 XX  
 XX  
 DT 10-SEP-2003 (first entry)  
 DE Human PRO1245 polypeptide.  
 XX  
 KW Human; PRO polypeptide; secreted protein; transmembrane protein;  
 KW genetic disorder; antibacterial; immunosuppressive.  
 XX  
 OS Homo sapiens.  
 XX  
 XX  
 PN US-002127576-A1.  
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 PD 12-SEP-2002.  
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 PF 14-NOV-2001; 2001US-00991073.  
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 PR 17-OCT-1997; 97US-0062250P.  
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 PR 12-NOV-1997; 97US-0065311P.  
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 PR 07-OCT-1998; 98WO-US021141.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030511.  
 PR 06-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
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 PR 22-FEB-2000; 2000WO-US004414.  
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 PR 24-FEB-2000; 2000WO-US005044.  
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 PR 20-MAR-2000; 2000WO-US014042.  
 PR 30-MAR-2000; 2000WO-US008439.  
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 PR 24-AUG-2000; 2000WO-US023338.  
 PR 08-NOV-2000; 2000WO-US030932.

PR 01-DEC-2000; 2000WO-US032678.  
 PR 28-FEB-2001; 2001WO-US006510.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-US0941992.  
 XX (GFTK ) GENENTECH INC.  
 XX PA  
 PR Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Godowski PJ, Gerritsen ME, Goddard A, Gerber H, Gerritsen N, Kjavin IJ, Napier MA, Pan J, Paoni NF, Grimaldi JC, Gurney AL, Roy MA, Stewart TA, Thomas D, Watanabe CK, Williams PM, Wood WI;  
 PI Zhang Z;  
 XX PT  
 PR Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO375, which stimulate proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune responses.  
 XX PT  
 PR Claim 12; Fig 290; 661pp; English.  
 XX PS  
 PR The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides for linking biactive molecules to cells expressing PRO polypeptides, for modulating biological activities of cells expressing PRO polypeptides, and for for identifying agonists or antagonists. The polynucleotide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals, or knockout animals, to construct hybridisation probes for mapping the gene which encodes the PRO polypeptide, and for the genetic analysis of individuals with genetic disorders, in gene therapy, for chromosome identification, as chromosome markers, and for generating probes for PCR, Northern analysis, Southern analysis and Western analysis. ABO25891-ABO5037 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at seqdata.uspto.gov/pstpdidntry.html.  
 XX SQ Sequence 104 AA;  
 PR Query Match 100.0%; Score 502; DB 6; Length 104;  
 PR Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
 PR Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 PR Qy 1 MKLALLGLCVTALSSSAARFLVGSAKPVHQPVVALESAAAGCCTLANPLGTNPLKL 60  
 PR Db 1 MKLALLGLCVTALSSSAARFLVGSAKPVHQPVVALESAAAGCCTLANPLGTNPLKL 60  
 PR Qy 61 LSSLGIPVNHLIEGSOKCYAELGPDAVAYKALKLGAITVFG 104  
 PR Db 61 LSSLGIPVNHLIEGSOKCYAELGPDAVAYKALKLGAITVFG 104  
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 XX RESULT 15:  
 PR ABU59026  
 PR ID ABU59026 standard; protein; 104 AA.  
 PR XX AC ABU59026;  
 PR DT 16-APR-2003 (first entry)  
 PR XX DE Human secreted/transmembrane protein, #163.  
 PR XX KW Human PRO; secreted; transmembrane; signal peptide; pharmaceutical;  
 PR KW diagnostic; biosensor; bioreactor; tumour; therapeutic; colon cancer;  
 PR KW lung cancer; breast cancer; gene therapy.  
 PR XX

OS Homo sapiens.  
 XX US2002112961-A1.  
 PN PR 03-OCT-2002.  
 PD XX 19-NOV-2001; 2001US-00989721.  
 PF XX 16-JUN-1997; 97US-0046787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
 PR 12-NOV-1997; 97US-06518P.  
 PR 13-NOV-1997; 97US-0065311P.  
 PR 14-NOV-1997; 97US-0066770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
 PR 28-APR-1998; 98US-0083322P.  
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 PR 28-MAY-1998; 98US-0087106P.  
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 PR 04-JUN-1998; 98US-0088030P.  
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 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
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 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
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 PR 16-DEC-1999; 99WO-US031095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.

PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US03565.  
 PR 18-FEB-2000; 2000WO-US04341.  
 PR 22-FEB-2000; 2000WO-US04414.  
 PR 24-FEB-2000; 2000WO-US05004.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 10-MAR-2000; 2000WO-US06319.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 20-MAR-2000; 2000WO-US07377.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US02031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 24-AUG-2000; 2000WO-US023328.  
 PR 08-SEP-2000; 2000WO-US010952.  
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 PR 01-OCT-2000; 2001WO-US01800.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019692.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001US-00941992.  
 XX (GETH ) GENENTECH INC.  
 XX PT New secreted and transmembrane PRO polypeptides (e.g. PRO193, PRO194, PRO361 or PRO846) useful as targets for therapeutic intervention in cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
 XX PT PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Godowski PJ; PI Perera N, Fong S, Gerber H, Gerritsen ME, Godowski PJ, Paoni NF; PI Grimaldi JC, Gurney AL, Klaivin JI, Napier MA, Pan J, Roy MA, Stewart TA, Tomas D, Watanabe CK, Williams PM, Wood WI; PI Zhang Z;  
 XX DR WPI, 2003-155950/15.  
 XX XX The invention discloses isolated PRO secreted/transmembrane polypeptides comprising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polynucleotides are also useful pharmaceuticals, diagnostics, biosensors or bioreactors, for detecting or treating e.g. tumours in mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs or rabbits as targets for therapeutic intervention in certain cancers (e.g. colon, lung or breast cancers) and diagnostic determination of the presence of these cancers. The PRO polypeptides are also useful as molecular weight markers or for chromosome identification. The PRO genes are useful as hybridisation probes or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. The sequences presented in ABU58900-ABU59046 are the PRO polypeptides of the invention  
 XX SQ Sequence 104 AA:  
 Query Match Score 502; DB 6; Length 104;  
 Best Local Similarity 100.0%; Pred No. 1, 4-e-48;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLALIGICVAAISCCSSAAGFLGSAKPVQAQPVALESAAEAGTIANPLGTINPLKL 60  
 Db 1 MKLALIGICVAAISCCSSAAGFLGSAKPVQAQPVALESAAEAGTIANPLGTINPLKL 60

Thu Jun 3 10:25:05 2004

us-09-700-770-9.rag

Page 17

Qy 61 LSSLGIPYNHLIEGSQKCVAEELGPQAVGAVKALKALLGALTVEG 104  
Db 61 LSSLGIPYNHLIEGSQKCVAEELGPQAVGAVKALKALLGALTVEG 104

Search completed: June 2, 2004, 20:19:02  
Job time : 25.778 secs

Result No.	Score	Query	Match	Length	DB	ID	Description
<b>SUMMARIES</b>							
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1	2238	100.0	420	4	QBWD9	Q8c243	mus musculu
2	1887	84.3	450	4	Q9UHB3	Q21966	caenorhabdi
3	1566	70.0	420	11	Q9QX71	Q86qi4	ancyllostoma
4	1551.5	69.3	419	11	Q9DCS8	Q8wr56	apricola ger
5	1550.5	69.3	419	11	Q9JTM79	Q9N9H3	necator aine
6	11025	45.8	399	13	Q93458	Q805f2	xenopus lae
7	1018.5	45.5	398	13	Q8JH28	Q804z9	xenopus lae
8	1018.5	45.5	398	13	Q8AWD9	Q95va2	clonorchis
9	1014.5	45.3	398	13	P87370	Q804z3	schistosoma
10	1005.5	44.9	399	13	Q9V313	Q805F2	schistosoma
11	1005.5	44.9	396	13	Q9DD89	Q804z3	oryza sativ
12	985.5	44.0	396	13	Q93428	Q805F3	oryza sativ
13	972.4	43.7	397	13	Q9W6D4	Q805F3	oryza sativ
14	974	43.5	395	13	Q8JT24	Q805F3	oryza sativ
15	966.5	43.2	385	5	Q721E4	Q805F3	oryza sativ
16	949.5	42.4	386	6	Q9BGU5	Q805F3	oryza sativ
<b>ALIGNMENTS</b>							
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	Gapext 0.0 , Gapext 0.5						
Searched:	US-09-700-770-8						
Total number of hits satisfying chosen parameters:	1017041						
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Maximum DB seq length:	2000000000						
Post-processing:	Minimum Match 0%						
	Maximum Match 100%						
	Listing first 45 summaries						
Database :	SPTREMBL 25::*						
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	2: sp_bacteria:*						
	3: sp_fungi:*						
	4: sp_human:*						
	5: sp_invertebrate:*						
	6: sp_mammal:*						
	7: sp_mhc:*						
	8: sp_organelle:*						
	9: sp_phage:*						
	10: sp_plant:*						
	11: sp_rabbit:*						
	12: sp_virus:*						
	13: sp_vertebrate:*						
	14: sp_unclassified:*						
	15: sp_tvirus:*						
	16: sp_bacteriophage:*						
	17: sp_archaea:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.							
Query Match	100.0%	Score 2238;	DB 4;	Length 420;			
Best Local Similarity	100.0%	Preid. No. 2e-171;					
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QY	61	PGDKP1FVPLSNYRVDVOYFGEIGLGPONFTVAFDTGSSNLWPSRRCHFFSVPCLWHH	120		61	PGDKP1FVPLSNYRVDVOYFGEIGLGPONFTVAFDTGSSNLWPSRRCHFFSVPCLWHH	120
Db	61	PGDP1FVPLSNYRVDQYFGEIGLGPONFTVAFDTGSSNLWPSRRCHFFSVPCLWHH	120		121	RFDPKASSFOANGTKFAIYQGTGRDGVILSEDKLTIGIKGASVIFGEALMWPSPLYPAF	180
Db	121	RFDPKASSFOANGTKFAIYQGTGRDGVILSEDKLTIGIKGASVIFGEALMWPSPLYPAF	180		121	RFPNASSFSKFGSGTAKIYQGTGRDGVILSEDKLTIGIKGASVIFGEALMWPSPLYPAF	180
QY	121	RFDPKASSFOANGTKFAIYQGTGRDGVILSEDKLTIGIKGASVIFGEALMWPSPLYPAF	180		181	AHDGDLGLGEPFLSVRGVRPPMDVLYVEQGLLDKPKVPSFYLNRDPEPDGGELVLGGSDP	240
Db	121	RFDPKASSFOANGTKFAIYQGTGRDGVILSEDKLTIGIKGASVIFGEALMWPSPLYPAF	180		181	SRPDGLLGEPFLSVRGVRPPMDVLYVEQGLLDKPKVPSFYFQRDPEADGGELVLGGSDP	240
QY	181	AHDGDLGLGEPFLSVRGVRPPMDVLYVEQGLLDKPKVPSFYLNRDPEPDGGELVLGGSDP	240		241	AHYIPPLTFVPTVPAWQIHMERVKVGQPLTLCKGAAILDGTSLITGPTEIRALH	300
Db	181	AHDGDLGLGEPFLSVRGVRPPMDVLYVEQGLLDKPKVPSFYLNRDPEPDGGELVLGGSDP	240		241	AHYIPPLTFVPTVPAWQIHMERVKVGQPLTLCKGAAILDGTSLITGPTEIRALH	300
QY	241	AHYIPPLTFVPTVPAWQIHMERVKVGQPLTLCKGAAILDGTSLITGPTEIRALH	300		301	AAIGGIPLLAGEYTILCSEIPKLPAVSPFLGGWFLNTAHDVYQFTRNGVBLCLSGFQA	360
Db	241	AHYIPPLTFVPTVPAWQIHMERVKVGQPLTLCKGAAILDGTSLITGPTEIRALH	300		301	AAAGGIPLLAGEYTILCSEIPKLPAVSPFLGGWFLNTAHDVYQFTRNGVBLCLSGFQA	360
QY	301	AAAGGIPLLAGEYTILCSEIPKLPAVSPFLGGWFLNTAHDVYQFTRNGVBLCLSGFQA	360		361	LDVPPAGPFWLGDVFEGTGYVAFDRGDMKSSARGVGLARTRGADIGWGETAQAOQPG	420
Db	301	AAAGGIPLLAGEYTILCSEIPKLPAVSPFLGGWFLNTAHDVYQFTRNGVBLCLSGFQA	360		361	LDVPPAGPFWLGDVFEGTGYVAFDRGDMKSSARGVGLARTRGADIGWGETAQAOQPG	420
QY	361	LDVPPAGPFWLGDVFEGTGYVAFDRGDMKSSARGVGLARTRGADIGWGETAQAOQPG	420				
Db	361	LDVPPAGPFWLGDVFEGTGYVAFDRGDMKSSARGVGLARTRGADIGWGETAQAOQPG	420				
<b>RESULT 3</b>							
		Q9QX71			PRELIMINARY;		
		ID	Q9QX71;		PRT;		
		AC	Q9QX71;		420 AA.		
		DT	01-MAY-2000 (TREMBLrel. 13, Created)				
		DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
		DT	01-MAY-2000 (TREMBLrel. 13, Last annotation update)				
		DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)				
		DE	NAP.				
		GN	Rattus norvegicus (Rat).				
		OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.				
		OC					
		NCBI_TaxID	10116;				
		OX					
		RN	[1]				
		RP	SEQUENCE FROM N.A.				
		RX	MEDLINE=20461778; PubMed=10958550;				
		RA	Schauer-Yukasnovic V., Wright M.B., Breu V., Giller T.; "Cloning, expression and functional characterization of rat napsin."				
		RT	Biochim. Biophys. Acta 1492:207-210(2000).				
		RL	"SIMILARITY: BELOWSKI, BELONGS TO PEPTIDASE FAMILY A1.				
		CC	EMBL; AJ251299; BELOWSKI, BEL265392; 1, -.				
		DR	HSSP; P00197; 2REN.				
		DR	MEROPS; A01_049; -.				
		DR	GO; GO:0004194; F:pepsin A activity; IFA.				
		DR	GO; GO:0008233; F:peptidase activity; IFA.				
		DR	InterPro; IPR001969; Asprotease and peptidolysis; IFA.				
		DR	InterPro; IPR001461; Peptidase_A1.				
		DR	InterPro; IPR000907; Pept_A_acid.				
		DR	Pfam; PF00026; asp; 1.				
		DR	PRINTS; PR000792; PEPSIN.				
		DR	PROSITE; PS00144; ASP PROTEASE; 2.				
		DR	Aspartyl Protease; Hydrolase; Protease.				
		SQ	SEQUENCE 420 AA; 45629 MW; B7731C85E106C0DD CRC64;				
		QY	1 MSPPPLQPLILLPLINNEPGATLIRIPLHRVQPGRTINLRGMWREPAAELPKLGAPS	60	70.0% Score 1566; DB 11; Length 420;		
		DR	MSPPPLQPLILLPLINNEPGATLIRIPLHRVQPGRTINLRGMWREPAAELPKLGAPS	60	Best Local Similarity 70.4%; Pred. No. 1.9e-117; Mismatches 39; Minmatches 299; Conservative 39; Gaps 5;		
		QY	1 MSPPPLQPLILLPLINNEPGATLIRIPLHRVQPGRTINLRGMWREPAAELPKLGAPS	60	60 SPQDPLFVPLISNYRDQYFEGIGLGPONFTVAFDTGSSNLWPSRRCHFFSVPCLWHH	119	
		DB	1 MSPPPLQPLILLPLINNEPGATLIRIPLHRVQPGRTINLRGMWREPAAELPKLGAPS	60	60 SPQDPLFVPLISNYRDQYFEGIGLGPONFTVAFDTGSSNLWPSRRCHFFSVPCLWHH	115	
		QY	61 PGDKP1FVPLSNYRVDQYFGEIGLGPONFTVAFDTGSSNLWPSRRCHFFSVPCLWHH	120	120 HRFDPKASSFOANGTKFAIYQGTGRDGVILSEDKLTIGIKGASVIFGEALMWPSPLYPAF	179	
		DB	61 PGDKP1FVPLSNYRVDQYFGEIGLGPONFTVAFDTGSSNLWPSRRCHFFSVPCLWHH	120	116 HRFNPKAASSFRPNQTKPAIQGTGRSLRSRNLTIGGIHNVSVTGFGEALWEPSPLYPAF	175	





DR	GO:0004194; F:pepsin A activity; EA.	Query Match	45.5%;	Score 1018.5;	DB 13;	Length 398;	
DR	Go: Go-000548; F:proteolysis and peptidolysis; IEA.	Best Local Similarity	50.5%;	Pred. No. 1.6e-73;			
DR	InterPro: IPR001969; Approtease AS.	Mismatches	65;	Matches 195;	Conservative	65;	
DR	InterPro: IPR001461; Peptidase_A1.	Indels	15;	Gaps	4;		
DR	InterPro: IPR00026; aspi; 1.						
PFam	PF00026; aspi; 1.	Qy	26 LIRIPLHRVQPGERTLNILRGWRPAAEP-----KLGAPPGDPBP1FVPLSNTYDVG 77				
PRINTS	PR00792; PPSNIN.	Db	19 TVRPLKKFTRLRLS -DSGRSLEELVSSNSNLKYNLGFASND -PTPETLKNYLDQA 75				
PROSITE	PS00141; ASP_PROTEASE; 2.	Qy	78 YFGBIGLGTTPONETVAFDTGSSNLWPSRRCHEFFSYCWCMLHFRDPKAASSFOANGTKF 137				
KW	SIGNAL; Hydrolase.	Db	76 YYEGIGLGPVQFTVFDTGSSNLWPSVHSLSLTDACLLRHKYNGCSSTYVNGTQF 135				
FT	SEQUENCE 398 AA; 43171 MW; 2A42FE2439B897F6 CRC64;	Qy	138 AIQYGTGRVDGILSEDKLTTGGTAKGASYVFGREALWPSLVEFAFAHDFGILGIGFPILSVE 197				
Best Local Similarity	45.5%;	Db	136 AIQYGSGLSGTYSQDCTGIDAVEKQIFGRAIKQCPVAFIAAKFCILGNAYPRAVD 195				
Matches 195;	Conservative	50.5%;	Db	136 AIQYGTGRVDGILSEDKLTTGGTAKGASYVFGREALWPSLVEFAFAHDFGILGIGFPILSVE 197			
Pred. No. 1.6e-73;	Mismatches	111;	Indels	15;	Gaps	4;	
SEQUENCE 398 AA;	43171 MW;	Qy	198 GVRPPMDVLYEQQLDKPFSYLNRDPEPDGGELVIGSDPAHYIPPLTFVPTVTPAY 257				
2A42FE2439B897F6 CRC64;		Db	196 GVPVFEDMMMSQKKEVNVFSEYLNRPDTQGGBLLGGTDPKYTGDENYVDISRQAY 255				
Qy	26 LIRIPLHRVQPGERTLNILRGWRPAAEP-----KLGAPPGDPBP1FVPLSNTYDVG 77	Qy	258 WQIHMERVYKVGPSLTLCKGCAAILDTGTSLITGPTETIRALHAAGGIPPLAGEYTILC 317				
Db	19 TVRPLKKFTRLRLS -DSGRSLEELVSSNSNLKYNLGFASND -PTPETLKNYLDQA 75	Db	256 WQHMDGMSIGSSLSLCKGGCAEVTDGTSLITGPAAEVKAIPLMGEMVDC 315				
Qy	78 YFGBIGLGTTPONETVAFDTGSSNLWPSRRCHEFFSYCWCMLHFRDPKAASSFOANGTKF 137	Qy	318 SEIPKLPAVSELIGGGWNFLNTADYVQTTRNGVRLCLSGEQALDYPHPFWILGDVF 377				
Db	76 YYEGIGLGPVQFTVFDTGSSNLWPSVHSLSLTDACLLRHKYNGCSSTYVNGTQF 135	Db	316 KKVPLPTISFSQGGVYSLGEQVYKQFGEBAIKQGFAIKFGLGNAYPRAVD 195				
Qy	138 AIQYGTGRVDGILSEDKLTTGGTAKGASYVFGREALWPSLVEFAFAHDFGILGIGFPILSVE 197	Qy	316 KKVPLPTISFSQGGVYSLGEQVYKQFGEBAIKQGFAIKFGLGNAYPRAVD 195				
Db	136 AIQYGSGLSGTYSQDCTGIDAVEKQIFGRAIKQCPVAFIAAKFCILGNAYPRAVD 195	Db	316 KKVPLPTISFSQGGVYSLGEQVYKQFGEBAIKQGFAIKFGLGNAYPRAVD 195				
Qy	198 GVRPPMDVLYEQQLDKPFSYLNRDPEPDGGELVIGSDPAHYIPPLTFVPTVTPAY 257	Qy	378 LGTYVAVPDRGDMKSARVGLARAT 403				
Db	196 GVPVFEDMMMSQKKEVNVFSEYLNRPDTQGGBLLGGTDPKYTGDENYVDISRQAY 255	Db	376 IGQYXTVFR---ENNRYGEFAKAKS 397				
Qy	258 WQIHMERVYKVGPSLTLCKGCAAILDTGTSLITGPTETIRALHAAGGIPPLAGEYTILC 317	RESULT 9					
Db	256 WQHMDGMSIGSSLSLCKGGCAEVTDGTSLITGPAAEVKAIPLMGEMVDC 315	ID	PB7370	PRELIMINARY;	PRT;	398 AA.	
Qy	318 SEIPKLPAVSELIGGGWNFLNTADYVQTTRNGVRLCLSGEQALDYPHPFWILGDVF 377	AC	PB7370;				
Db	316 KKVPLPTISFSQGGVYSLGEQVYKQFGEBAIKQGFAIKFGLGNAYPRAVD 195	DT	01-MAY-1997 (TREMBLrel. 03, Created)				
Qy	318 SEIPKLPAVSELIGGGWNFLNTADYVQTTRNGVRLCLSGEQALDYPHPFWILGDVF 377	DT	01-OCT-2003 (TREMBLrel. 03, Last annotation update)				
Db	316 KKVPLPTISFSQGGVYSLGEQVYKQFGEBAIKQGFAIKFGLGNAYPRAVD 195	DE	Cathepsin D (EC 3.4.23.5).				
Qy	378 LGTYVAVPDRGDMKSARVGLARAT 403	OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).				
Db	376 IGQYXTVFR---ENNRYGEFAKAKS 397	RL	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Buteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.				
RESULT 8		CC	-! SIMILARITY: BELONGS TO PEPTIDASE FAMILY A1.				
QBAND9	PRELIMINARY;	DR	EMBL; U90321; AAC60301.1; -.				
ID	PRT;	DR	HSSP; P07339; 11YB.				
QBAND9;	PRELIMINARY;	DR	NCBI_TaxID:9022; -.				
AC	PRT;	DR	MEICOPS; A01_009; -.				
DT	01-MAR-2003 (TREMBLrel. 23, Created)	DR	GO; GO:0004192; F:cathepsin D activity; IEA.				
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)	DR	GO; GO:0004194; F:pepsin A activity; IEA.				
RA	Similar to cathepsin D.	RA	GO; GO:0008233; F:peptidase activity; IEA.				
DR	Brachydanio rerio (Zebrafish) (Danio rerio).	RL	"Molecular characterisation of ovarian cathepsin D in the rainbow trout, Oncorhynchus mykiss.";				
OS	Actinopterygii; Neopterygii; Chondriata; Craniata; Vertebrata; Euteleostomi; Cyprinidae; Danio.	DR	Gene 20:45-54 (1997).				
OC	Cyprinidae; Danio.	DR	DR InterPro; IPRO01461; Peptidase_A1.				
OC	Cyprinidae; Danio.	DR	DR InterPro; IPRO01461; Peptidase_A1.				
OX	NCBI_TaxID:7955;	DR	DR InterPro; IPRO0026; ASP; 1.				
RN	SEQUENCE FROM N.A.	DR	DR InterPro; IPRO0026; ASP; 1.				
RP	SEQUENCE FROM N.A.	DR	DR InterPro; IPRO0026; ASP; 1.				
Strasbourg R.	Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.	DR	DR InterPro; IPRO0026; ASP; 1.				
RA	GO; GO:0006508; F:pepsin A activity; IEA.	DR	DR InterPro; IPRO0026; ASP; 1.				
RL	DR InterPro; IPRO01461; Peptidase_A1.	DR	DR InterPro; IPRO0026; ASP; 1.				
DR	InterPro; IPRO01461; Peptidase_A1.	DR	DR InterPro; IPRO0026; ASP; 1.				
DR	InterPro; PS00141; ASP_PROTEASE; 2.	DR	DR InterPro; IPRO0026; ASP; 1.				
DR	PROSITE; PS00141; ASP PROTEASE; 2.	DR	DR InterPro; IPRO0026; ASP; 1.				
DR	SEQUENCE 398 AA; 43199 MW; 2EB897840DE5AD6 CRC64;	DR	DR InterPro; IPRO0026; ASP; 1.				
SQ	SEQUENCE 398 AA;	DR	DR InterPro; IPRO0026; ASP; 1.				
Query Match	45.3%;	DR	DR InterPro; IPRO0026; ASP; 1.				
Best Local Similarity	50.6%;	DR	DR InterPro; IPRO0026; ASP; 1.				
Pred. No. 3.4e-73;		DR	DR InterPro; IPRO0026; ASP; 1.				

Matches	195;	Conservative	64;	Mismatches	113;	Gaps	3;
QY	26	LIRIPLHRVQGRRTL-----NULRGWREPAELPKLGAPSPGDKPIFVPLSNYRDVQ	77				
Db	19	LVRIPLRKFRSIRRTLTDGRAEEELAG-QEHTKYNNLGPSSNSGTPETLXNFMDAQ	77				
QY	78	YFGEGIIGLTPQNFTVAFDTGSNNLWVPSRRCFFPSVCPWLHFRDPKAASSFOQANTKF	137				
Db	78	YYGEGLGPVQTFVTFDTCSSNLWVPSVHCSFTIACLJLHKYNGAKSTSYYVNGTAF	137				
QY	138	AIQYGGTGRVGILSEDKLTIGGIKGASVIFGEALWPSLVEFAAHFDGLGFPILSV	197				
Db	138	AIQYGGSGSLGYSQDTCITGSLIEDQGFGEAKOFGVATAAKEDGIGLMAYPRISD	197				
QY	198	GYRPMPMDVLYEQGLLDKPVFESFYLNDRPEPDGGELVGGSDPAHYIPLPTFVPTVVPAY	257				
Db	198	GVAPPFDNTMSQKQKVQEONVFSFYLNENPDSBPGGEILGGTDPKYSGDFQYLDVSRQAY	257				
QY	258	WQIHAMERVKVPGGLTLCAGGAIDTGTSLITGPEETIRALHAAGGTPPLAGEYTILC	317				
Db	258	WQIHMDCGMVGSFLSSLCKGGCAIVDTGTSLITGPAAEVKAQLQRAIGATPLIQGEMYN	317				
QY	318	SEIPIKLPVASFVLLGWWFVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWVWV	377				
Db	318	DRIPIRMVITFLNGLGGOSYLTAEQYVIREQSAGKTICLISGFNGLDPAPAGLWLIGDV	377				
QY	378	LGTYVAVFDRGDMKSSARVGLALAR	402				
Db	378	TGQQYTFVDR---DNTRGFAKSK	398				
RESULT 10							
ID	Q9V313	PRELIMINARY;	PRT;	392 AA.			
AC	Q9V313;						
DT	01-MAY-2000 (T=EMBL[re])	13;	Created				
DT	01-OCT-2000 (T=EMBL[re])	13;	Last sequence update				
CG	1548	protein (SD07085P).					
DE	CATHD OR CG1548.						
OS	Drosophila melanogaster (fruit fly).						
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.						
NCBI_TaxID	7227;						
RN	[1]						
SEQUENCE FROM N.A.							
STRAIN-Berkeley;							
MEDLINE=20196006; PubMed=10731132;							
RA	Adams M.D., Cejnikova S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.B., Richards S., Ashburner M., Henderson S.N., Sutton B.G., Wormit J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blaeze R.G., Champre M., Peiffer B.D., Wan K.H., Doyle C., Baxter E.G., Heit G., Neilson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrew-Pfankoch C., Baldwin D., Ballew R.M., Basu A., Baxendale J., Bayraktarocali L., Beasley E.M., Beeson K.Y., Bens P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P., Burritis K.C., Busam D.N., Butler H., Cadieu E., Center A., Chandra I., Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S. M., Dodson K., Doupe J.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., Durbin R.J., Evangelista C.C., Ferrara S., Fleischmann W., Fosler C., Gabrielsson A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Hernandez T.J.R., Houck J., Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ikegami C., Jalali M., Kalush P., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., Kimmei B.B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Liu X., Matveev T.C., McCallion M., McCallion M., McPherson D., Merkulov G., Milashina N.V., Mobarry C., Morris J.J., Moshirei A., Munkres J., Nelson D.M., Nelson D.L., Nusslein K., Pollard J., Puri V., Reesee M.G., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reesee M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Strong R., Sun E., Spier B., Spradling A.C., Stapleton M., Strickland J., Turner B., Wang A.H., Wang X., Svirbielas R., Tector C., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh P.-F., Zaveri J.S., Zhan M., Zhang G., Zheng L., Zheng X.H., Zhong P.N., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT The genome sequence of <i>Drosophila melanogaster</i> .; RT "The genome sequence of <i>Drosophila melanogaster</i> .;"						
RA	Mount S.M., Moy M., Murphy B., Murphy L., Munyan D.M., Nelson D.L., Nelson D.R., Nelson K.A., Nixon J., Nusslein D.R., Paciebiek J.M., Reesee M.G., Reinert K., Remington K., Saunders R.D.C., Scheeler P., Shen H., Shue B.C., Siden-Kiamos I., Skupski M.P., Smith T., Spier B., Spradling A.C., Stapleton M., Strickland J., Turner B., Wang A.H., Wang X., Svirbielas R., Tector C., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh P.-F., Zaveri J.S., Zhan M., Zhang G., Zheng L., Zheng X.H., Zhong P.N., Zhou X., Zhu S., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; RT The genome sequence of <i>Drosophila melanogaster</i> .;"						
RA	Scienc 287:2185-2195(2000).						
RA	[2]						
RA	RP SEQ JENCE FROM N.A.						
RA	RP PAGE A.W., Tsang G., Rubin G.M.; RT "A <i>Drosophila</i> gene related to cathepsin D."; RT Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.						
RA	RL RNAME FROM N.A.						
RA	RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champ M., Chavez C., Dorsett V., Farooq D., Frise E., George R., Gonzalez M., Guarini H., Li P., Liao G., Miranda A., Mangall C.J., Nunoo J., Paciebiek J., Paradas V., Park S., Photanenavong S., Wan K., RA Yeh C., Lewis S.E., Rubin G.M., Celinkin S.; RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.						
RA	RL - SIMILARITY: BELONGS TO PEPTIDE FAMILY A1.						
CC	CC DR PRINTS; PF00026; apri 1.						
CC	DR EMBL; AF220040; AAF59186.1; -.						
CC	DR EMBL; AY052119; AAK93543.1; -.						
DR	DR MEROPS; A01_009; -.						
DR	DR FLYBase; FBgn0029093; cathd.						
DR	DR GO; GO_0000233; F:peptidase activity; IEA.						
DR	DR GO; GO_0000233; F:peptidase activity; IEA.						
DR	DR GO; GO_0006508; P:proteolysis and peptidolysis; IEA.						
DR	DR InterPro; IPR001969; Aspartyl protease AS.						
DR	DR InterPro; IPR001461; Peptidase AI.						
DR	DR InterPro; IPR003007; Pept_A_acid.						
DR	DR Pfam; PF00026; apri 1.						
DR	DR PRINTER; PR00092; PEPSIN.						
DR	DR PROSITE; PS01041; ASY_PROTEASE; 2.						
KW	KW Aspartyl protease; Hydrolase; Protease.						
SQ	SQ 392 AA; 42472 MM; 022E/F5C09BB43F4 CRC64;						
SEQUENCE	SEQUENCE FROM N.A.						
Q9V313	Q9V313 PRELIMINARY; PRT; 392 AA.						
QY	01-MAY-2000 (T=EMBL[re])	13;	Created				
DT	01-OCT-2003 (T=EMBL[re])	25;	Last annotation update				
CG	CG1548 protein (SD07085P).						
GN	CATHD OR CG1548.						
OS	Drosophila melanogaster (fruit fly).						
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.						
NCBI_TaxID	7227;						
RN	[1]						
RA	Best Local Similarity 44.9%; Score 1005.5; DB 5; Length 392; Matches 191; Conservative 56; Mismatches 112; Indels 25; Gaps 6						
RA	RA 26 LIRIPLHRVQGRRTL-----NULRGWREPAELPKLGAPSPGDKPIFVPLSNYRDVQ						
RA	RA 27 LIRVPLHRVQGRGR-----TLLNLRGSWRPAAELPKLGAPSPGDKPIFVPLSNYRDVQ						
QY	79 FGIGIGLTPPQNTFTVADTGSNNLWVSSRRCFFSVPVWLHFRDPKASSFOQANTKF						
DB	74 YGP1AIGSPQNPFRVVFPTGSSNLWVPSKKCHLNTIACLMENKDYASKSKTVTKNGTEFA						
QY	139 IOTYGTGRYDGILSLEDKLTTGGIKGASVIFGEALWPSLVEFAFAHDFGILGLGPFLSYEG						
DB	134 IQGSGSLGSYLTDTVSIAGLKDQTFAEALSSEPLGVVFKFDGLLGIGYNSISYDK						
QY	199 VRPPMDVLFVQSFYLDKPKVPSYLNRDPEPDGGENVLGGSDPAHYIPLTFVTPAYW						
DB	194 VCPFPYANVQEGIISAPVFSYLNRDPSPEGEBIIFGGSDPNHYTGERTYFLVTRKAYW						
QY	259 QIIMBERVKGPGIQLCAKGCAAIDTGTSLITGPTTEEIRALHAIGGPLLACEYIILCS						
DB	254 QIKMDAASIG-DLQCKGGCOVIAIDTGTSLIAAPLEBATSINOKIGTPPIQVYVSCD						
QY	319 EIPKLPAYSFLIGGCVWENLTAHDYVICTRNGYRLCLSGFOALDVPAPPFWLGDYFL						
DB	313 LIPLPVIKEVPLGKTFBEGDQYILRQAQMGIKCIUSGFMGJIDPPNGELWLGDFI						



Db	292	VEYRALQKAIGAFAPIIQLQGYMVNCITVPSLPIVISTVGGVYTLTGQYLILKVTDAKGKTM	351
Qy	354	CLSGFQALDVPPPPGFWLGDVFQFTYAVFDRDMKSSARVGLARAR	402
Db	352	CLSFMFGLDIPAPAGPLWLGDVFNGQYTFDR	--DIANRVGPAKAK
			396
	RESULT 13		
	Q9W6D4	PRELIMINARY:	PRT;
	ID	397 AA.	
	AC		
	Q9W6D4;		
	DT	01-NOV-1999 (TREMBUREL, 12; Created)	
	DT	01-NOV-1999 (TREMBUREL, 12; Last sequence update)	
	DT	01-OCT-2003 (TREMBUREL, 25; Last annotation update)	
	DE	Cathespin D (IUC 3.4.23.5).	
	OS	Hynobius leechii (Korean salamander).	
	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	OC	Amphibia; Batrachia; Caudata; Cryptobranchidae; Hynobiidae; Hynobius.	
	OX	NCBI_TaxID=113391;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RX	SEQUENCEID=0358712; PubMed=10902906;	
	RA	JU B.G., Kim W.S.;	
	RT	"Cloning of a cDNA encoding cathepsin D from Salamander, <i>Hynobius leechii</i> , and its expression in the limb regenerates."	
	RT	DNA Seq. 11:21-28 (2000).	
	RL	-!- SIMILARITY TO PEPTIDASE FAMILY A1.	
	CC	EMBL: AF115925; AAD3219.1; -.	
	DR	HSSP: P07339; ILYB.	
	DR	MEROPS; A01.000; -.	
	DR	GO; GO:0004192; F:cathepsin D activity; IEA.	
	DR	GO; GO:0004194; F:pepsin A activity; IEA.	
	DR	GO; GO:000833; F:peptidase activity; IEA.	
	DR	GO; GO:0006508; P:proteolysis and peptidolysis; IEA.	
	DR	InterPro: IPR001969; Approtease_AS.	
	DR	InterPro: IPR001461; Peptidase_A1.	
	DR	InterPro: IPR009007; Pept_A_acid.	
	DR	Pfam: PF00026; asp_1.	
	DR	PRION; PR00192; PEPSIN.	
	DR	PROSITE: PS00041; ASP PROTEASE; 2.	
	DR	Aspartyl protease; Hydrolase; Protease.	
	KW	SEQUENCE 39 AA; 42855 MW; 75CBLA4.8203DFE9 CRC64;	
	SQ	Query Match 43.7%; Score 977; DB 13; Length 397;	
		Best Local Similarity 48.3%; Prod. No. 3.5e-70;	
		Matches 194; Conservative 70; Mismatches 116; Indels 22; Gaps 5	
Qy	10	LJLLPLPLNLVEQSGATLRIPLRVRQPGRTINLGRGPAPAEPLKLGPSPGKPKPFLVP	69
Db	7	LILLAPILLAH--MYRIPLTKFRSIRTHLTEAGG----DVKNLYATSDQTKYNCPP	58
Qy	70	-----LSNYRDYQVFGEEIGGTGTPPNFTYAFDTGGSNNLWPSRRCHFFSVPCWLHH	120
Db	59	KTQQPTPTLILNLDQYHGEICGTGPPCFTVFDGSSNLWPSVHSLLDACLWHP	115
Qy	121	RDPKASSSFQANGTKEAIQYGTGRDGTLSEDPLLTIGTGTGASVIFGRALWEPSSLVFAF	180
Db	119	KYDSSSSTYVNGTEFQYQTSQGSLGTLRQDGTYTFDNIMQSXVKEKNVFSYLNRPNDTRPGEGLLGTDP	231
Qy	181	AHYPPPLTFPVPTVTPAYWQHMRVYKVGPLTLCAKGAAILDGTSLITGPTEIRALH	300
Db	179	AKEDGILGMAYPRISVDGTYTFDNIMQSXVKEKNVFSYLNRPNDTRPGEGLLGTDP	244
Qy	241	NYTTGDFTFYLNTPRAYWQHMDQGVDGDLTLCGGCEALVDTGTSLSLIGPSALVLAQ	291
Db	239	AAIGIPLIQLAGEYILCSELPKLPAVSFLGGWWFNLTADHYVQTTRNGVRLCLSGFOA	361
Qy	301	KATGAIPLIQLQEGYMPCDKVPSPVTFNNGKATVSGDYYVQKVSQAGHTLGSMFGM	355
Db	299	LDVPPAGPEWILGDYFLGIVYAVDRGDKMSARVGLAR	402
Qy	361	LDVPPAGPEWILGDYFLGIVYAVDRGDKMSARVGLAR	355



Scoring table:	BLOSUM62				
Gapop:	10.0 , Gapext 0.5				
Searched:	141681 seqs, 52070155 residues				
Total number of hits satisfying chosen parameters:	141681				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100%				
Database :	SwissProt_42;*				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES	%				
Result No.	Score	Query Match	Length	DB ID	Description
1	2232	99.7	420	1 NAP1_HUMAN	096009 homo sapien
2	1560.5	69.7	419	1 KDAP_MOUSE	009043 mus musculus
3	1019.5	46.0	398	1 CATD_CHICK	Q05744 gallus gallus
4	1019.5	45.6	396	1 CATD_CLTHA	Q9dex3 clupea harengus
5	1015	45.4	412	1 CATD_HUMAN	P07339 homo sapien
6	1005	44.9	407	1 CATD_RAT	P24268 rattus norvegicus
7	992.5	44.3	410	1 CATD_MOUSE	P18242 mus musculus
8	967.5	43.2	390	1 CATD_BOVIN	P80209 bos taurus
9	964.5	43.1	387	1 ASPP_ASPPD	Q03168 aedes aegypti
10	944	42.2	345	1 CATD_PIG	P00795 sus scrofa
11	922.5	41.2	365	1 CATD_SHEEP	Q9mz88 ovis aries
12	878	39.2	397	1 CATE_MOUSE	P24796 mus musculus
13	869	38.8	396	1 CATE_HUMAN	P14091 homo sapiens
14	867	38.7	398	1 CATE RAT	P16228 rattus norvegicus
15	848.5	37.9	396	1 CATE_RABIT	P43159 orctotolagus
16	830	37.1	508	1 ASPR_HORVU	P42210 hordeum vulgare
17	808.5	36.1	401	1 RENS_MOUSE	P00796 mus musculus
18	806	36.0	391	1 CAVP_CAVPO	Q42456 orzyza sativa
19	804	35.9	509	1 APR1_ORYSA	P06281 ovis aries
20	797	35.6	402	1 REN1_MOUSE	P40782 cynara cardunculus
21	783	35.0	400	1 CYPL_CYNCA	P08424 rattus norvegicus
22	781	34.9	473	1 REN1_RAT	P00797 homo sapiens
23	779	34.8	402	1 REN1_RAT	P60016 pan troglodytes
24	779	34.8	406	1 REN1_HUMAN	P42211 orzyza sativa
25	779	34.8	406	1 REN1_PANTHER	O04057 cucurbita pepo
26	773.5	34.6	496	1 ASPR_ORYSA	P27678 macaca fasciata
27	769.5	34.4	513	1 ASPR_CUCPEL	P11489 macaca mulatta
28	767.5	34.3	388	1 PBP4_MACFUF	P00790 homo sapiens
29	765.5	34.2	388	1 PBP4_MACMUF	P27677 macaca fasciata
30	759.5	33.9	388	1 PBPA_HUMAN	P55956 caenorhabditis elegans
31	757.5	33.8	388	1 PBP2_MACFUF	P03954 macaca fasciata
32	756	33.8	398	1 ASP3_CAEEL	P04073 rattus norvegicus
33	755.5	33.8	388	1 PBP1_MACFUF	P18276 ovis aries

## ALIGNMENTS

RESULT 1	NAP1_HUMAN	STANDARD;	PRT;	420 AA.
ID	NAP1_HUMAN			
AC	O96109;			
DT	30-MAY-2000 (Rel. 39, Created)			
DT	30-MAY-2000 (Rel. 39, Last sequence update)			
DT	28-FEB-2003 (Rel. 41, Last annotation update)			
DE	Napsin 1 precursor (EC 3.4.23.-) (NAPSIN A) (NAPA) (TA01/TA02)			
DE	(Aspartyl protease 4) (ASP4) (ASP 4)			
GN	NAP1.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN				
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Kidney and Lung;			
RX	Medline=9909899; PubMed=9877162;			
RA	Ratnai L.P.J., Powell D.J.J., Hill J., Smith T.S., Tew D.G., Kay J.J.,			
RT	"Napsins: new human aspartic proteinases. Distinction between two closely related genes."			
RT	FEBs Lett. 44:43-48 (1998).			
RL				
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Liver;			
RA	Koeisch G., Wu S., Henthorn J., Tang J., Lin X.; New human aspartic proteinases napsin 1 and napsin 2: molecular cloning and intracellular localization of napsin 1."			
RT	Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.			
RL				
RN	[3]			
RP	SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MASS SPECTROMETRY.			
RC	TISSUE=Fetal lung;			
RX	Medline=20047840; PubMed=10580105;			
RA	Chunyan Y., Bergman A.-C., Ueno T., Saito S., Sakaguchi K., Alaya A.A., Franzen B., Bergman T., Arnott D., Auer G., Appella E., Joerntvall H., Lindner S.,			
RT	"Napsin A, a member of the aspartic protease family, is abundantly expressed in normal lung and kidney tissue and is expressed in lung adenocarcinomas"; FEBs Lett. 46:129-134 (1999).			
RL				
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Bienkowski M.J., Shuck M.E., Slightom J.L., Drong R.F., Submitt (OCT-1999) to the EMBL/GenBank/DDBJ databases.			
RL	- - FUNCTION: May be involved in processing of pneumocyte surfactant precursors.			
CC	- - TISSUE SPeCIFICITY: Expressed predominantly in adult lung (type II pneumocytes) and kidney and in fetal lung. Low levels in spleen and very low levels in peripheral blood leukocytes.			
CC	- - SIMILARITY: Belongs to Peptidase family A1.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial			

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CC	KDAP OR NAP.	GN	OS
CC	Mus musculus (Mouse).	OC	Batrachota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Eukaryota; Mammalia; Buteraria; Rodentia; Muridae; Murinae; Mus.	OC	
CC	NCB: TaxID=10909;	OX	
DR	EMBL; AF090386; AAD01917.1; -;	RN	[1]
DR	EMBL; AF098484; AAD13215.1; -;	RP	SEQUENCE FROM N.A.
DR	EMBL; AF200345; AAF17081.1; -;	RC	STRAIN=BALB/c; TISSUE=Kidney;
DR	HSSP; P00797; 2REN.	RX	Medline=97165991; PubMed=901890;
DR	MEROPS; A01_046; -;	RA	Mori K., Ogawa Y., Tamura N., Ebihara K., Aoki T., Muro S., Ozaki S.,
DR	GO; GO:0004190; F:aspartic-type endopeptidase activity; TAS.	RA	Tanaka I., Tasbilo K., Nakao K.,
DR	GO; GO:0006508; B:proteinolysis and peptidolysis; TAS.	RA	"Molecular cloning of a novel mouse aspartic protease-like protein that is expressed abundantly in the kidney.",
DR	InterPro; IPR001969; Asparte_AS.	RT	FEBs Lett. 401:218-222 (1997).
DR	InterPro; IPR000907; Pept_A_acid.	RT	
DR	InterPro; IPR001461; Peptidase_A1.	RL	
PFam; PF00026; ASP_1.	RN	[2]	
PRINTS; PR00792; PEPSIN.	RP	SEQUENCE FROM N.A.	
DR	PROSITE; PS00141; ASP PROTEASE_2.	RC	STRAIN=120334768; PubMed=11082105;
KN	Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.	RX	Medline=22388257; PubMed=12477932;
FT	SIGNAL 1 25 POTENTIAL.	RA	strauberg R.L., Feingold B.A., Grouse L.H., Derge J.G., Schuller G.D.,
FT	PROPEP 26 63 ACTIVATION PEPTIDE.	RC	Klauser R.D., Shemesh C.M., Wagner L., Peters C.,
FT	CHAIN 64 420 NAPSIN 1.	RX	Collins F.S., Zeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
FT	ACT SITE 96 96 BY SIMILARITY.	RA	Tateell P.J., Cook M., Peters C.,
FT	DISULFID 283 283 BY SIMILARITY.	RA	Altschul S.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
FT	DISULFID 109 116 BY SIMILARITY.	RA	Hopkins R.F., Farmer A.A., Rubin G.M., Hong L.,
FT	DISULFID 274 278 BY SIMILARITY.	RA	Diatchenko L., Marusina K., Casavant T.L., Scheetz T.E.,
FT	DISULFID 317 354 BY SIMILARITY.	RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Carninci P., Prange C.,
FT	CARBONYD 90 90 N-LINKED (GLCNAC. . .) (POTENTIAL).	RA	Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P.,
FT	CARBONYD 133 133 N-LINKED (GLCNAC. . .) (POTENTIAL).	RA	Raha S.S., Longellano P.J., Abramson R.D., Mullany S.J.,
FT	CARBONYD 336 336 N-LINKED (GLCNAC. . .) (POTENTIAL).	RA	Bosak S.A., McKernan P.J., McKernan P.H.,
SQ	SEQUENCE 420 AA; 45386 NW; 018B8AE5BD0C865 CRC64;	RA	Richard S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Db	1 MSPPPLQQLLPLPLNLVPEPGATLRLRPLHVRQPGRRTRNLRLGRMREPAAELPKLQGAPS 60	RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Db	1 MSPPPLQQLLPLPLNLVPEPGATLRLRPLHVRQPGRRTRNLRLGRMREPAAELPKLQGAPS 60	RA	Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,
Db	2 MSPPPLQQLLPLPLNLVPEPGATLRLRPLHVRQPGRRTRNLRLGRMREPAAELPKLQGAPS 60	RA	Whiting M., Madan A., Young A.C., Bouffard G.G.,
Qy	Best Local Similarity 99.7% Score 2322; DB 1; Length 420; Pred. No. 2_7e-172; Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Db	61 PGDKPITFPLSNTRDVQYGEIIGTGPQNFTVAFDTGSNNLWPSRSRCHFFSVPCKWHLH 120	RA	Rodriguez A.C., Grimwood J.J., Schmutz J., Myers R.M.,
Db	61 PGDKPITFPLSNTRDVQYGEIIGTGPQNFTVAFDTGSNNLWPSRSRCHFFSVPCKWHLH 120	RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Qy	1 RFDKMASSPQQANGTKFAQYGTGRVGDGLSEDKLTIKGKGSVIRGFBALWPSLVLQAF 180	RA	Schnerch A., Schein J.E., Jones S.J.M., Marrs M.A.; RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.",
Db	121 RFDKMASSPQQANGTKFAQYGTGRVGDGLSEDKLTIKGKGSVIRGFBALWPSLVLQAF 180	RT	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
Qy	181 AHFDGILGIGFPILSVEGVRPPMDVLYEQLDQKPVFSPYLNRDDEPDQGELNLGGSDP 240	CC	-1 TISSUE SPECIFICITY. Expressed at the highest levels in the kidney, at a moderate level in the lung, and at low levels in the spleen
Db	181 AHFDGILGIGFPILSVEGVRPPMDVLYEQLDQKPVFSPYLNRDDEPDQGELNLGGSDP 240	CC	and adipose tissue.
Qy	241 AHYIPPLTFPVTPYTPAYWQHMERVKGPGLTCAKGCAAILDTGTTGPEETIRALH 300	CC	-1 SIMILARITY: Belongs to peptidase family A1.
Db	241 AHYIPPLTFPVTPYTPAYWQHMERVKGPGLTCAKGCAAILDTGTTGPEETIRALH 300	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement. (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to license@isb-sib.ch).
Qy	301 AAIGGIPILLAGEYIIICSEPKLPAVSFLLGGWPNLTAHDYVQTTRNGVRLCLSGFOA 360	CC	CC DR EMBL; D88899; BAA19004.1; -
Db	301 AAIGGIPILLAGEYIIICSEPKLPAVSFLLGGWPNLTAHDYVQTTRNGVRLCLSGFOA 360	CC	CC DR EMBL; B014813; ARH14813.1; -
Qy	361 LDVPPPAAGPFWILGDYFLGTVAVFDGMKSSARVGLAPARTRGADLGGETAQAFPG 420	CC	CC DR EMBL; D88899; CAB82907.1; -
Db	361 LDVPPPAAGPFWILGDYFLGTVAVFDGMKSSARVGLAPARTRGADLGGETAQAFPG 420	CC	CC DR EMBL; A01_049; -
Qy	361 LDVPPPAAGPFWILGDYFLGTVAVFDGMKSSARVGLAPARTRGADLGGETAQAFPG 420	DR	MDG; MTG; 109365; KdAp.
Db	361 LDVPPPAAGPFWILGDYFLGTVAVFDGMKSSARVGLAPARTRGADLGGETAQAFPG 420	DR	InterPro; IPRO01969; APPROTEASE_AS.
DR	15-JUL-1999 (Rel. 38, Created)	DR	InterPro; IPRO01461; Peptidase_A1.
DR	15-MAR-2004 (Rel. 43, Last sequence update)	DR	Pfam; PF00026; ASP_1.
DE	Kidney-derived aspartic protease-like protein precursor (EC 3.4.23.-)	DR	PRINTS; PRO00732; PEPSIN.
DE	(KDAP-1) (KAP) (Napsin).	DR	PROSITE; PS00141; ASP_PROTEASE; 2.

RESULT 2

KDAP\_MOUSE  
ID KDAP\_MOUSE  
AC AC090733  
DT 15-JUL-1999 (Rel. 38, Created)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Kidney-derived aspartic protease-like protein precursor (EC 3.4.23.-)  
DE (KDAP-1) (KAP) (Napsin).



RESULT 4		CATD_CLOHA		STANDARD;		PRT;		396 AA.		
QY	CATD_CLOHA	AC	Q9DEX3; O9AC	DT	28-FEB-2003 (Rel. 41, Created)					
		DT		DT	(Rel. 41, Last sequence update)					
		DT		DT	10-OCT-2003 (Rel. 42, Last annotation update)					
		DE		DE	Cathepsin D precursor (EC 3.4.23.5).					
		OS		OS	Clupea harengus (Atlantic herring).					
		OU		OU	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupidae; Clupea.					
		OC		OC	NCBI_TaxID=7950;					
		OX		OX	[1] RN					
					SEQUENCE FROM N.A.					
					NIelsen L.B., Poulsen P., Andersen P.S., Pedersen L.H.;					
					"Cloning and sequence determination of herring muscle cathepsin D."					
					Submitted (OCT-2000) to the EMBL/GenBank/DDJB databases.					
					[2]					
					SEQUENCE OF 62-82.					
					TISSUE=Skeletal muscle;					
					MEDLINE=21165459; PubMed=11207447;					
					RA Nielsen L.B., Nielsen H.H.;					
					RT "Purification and characterization of cathepsin D from herring muscle (Clupea harengus).";					
					Comp. Biochem. Physiol. 128B:351-363(2001).					
					-1- FUNCTION: Cathepsin D is an acid protease active in intracellular protein breakdown.					
					-1- CATALYTIC ACTIVITY: Specificity similar to, but narrower than, that of peptidase A. Does not cleave the 4-Gln-[His-5 bond in B chain of insulin.					
					-1- ENZYME REGULATION: Inhibited by pepstatin.					
					-1- SUBUNIT: Monomer.					
					-1- SUBCELLULAR LOCATION: Lysosomal.					
					-1- MISCELLANEOUS: The isoelectric point is 6.8. Has optimal activity at pH 2.5 with hemoglobin as the substrate and the optimal temperature is 37 degrees Celsius.					
					-1- SIMILARITY: Belongs to peptidase family Al.					
					-----					
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					-----					
					CC EMBL; AF312364; ANG27733.1; - .					
					CC HSSP; P07339; ILYB.					
					DR MEROPS; A01_009; - .					
					DR InterPro; IPR001969; Asprotease_AS.					
					DR InterPro; IPR009007; Pept_A_acid.					
					DR InterPro; IPR001461; Peptidase_Al.					
					DR Pfam; PF00026; asp; 1 .					
					DR PRINIS; PRO00792; PEPSIN.					
					DR PROSITE; PS00141; ASP_Protease; 2 .					
					FT HYDROLASE; Aspartyl_protease; Glycoprotein; Lysosome; Sigmaal; Zymogen.					
					FT SIGNAL 1 18 POTENTIAL.					
					FT PROPEP 19 61 ACTIVATION PEPTIDE.					
					FT CHAIN 62 396 CATHEPSIN D.					
					FT ACT_SITE 94 94 BY SIMILARITY.					
					FT ACT_SITE 281 281 BY SIMILARITY.					
					FT DISULFID 107 114 BY SIMILARITY.					
					FT DISULFID 272 276 BY SIMILARITY.					
					FT DISULFID 315 352 BY SIMILARITY.					
					FT CARBOHYD 131 131 N-LINKED (GLCNAC-. . .) (POTENTIAL).					
					SQ SEQUENCE 396 AA; 43315 MW; D0375D3856A31B CRC64; .					

Query Match	45 68;	Score 1019 5;	DB 1;	Length 396;
Best Local Similarity	50 68;	Pred. No. 1.1e-74;		
Matches	196;	Conservative	62;	Nimatches 108;
		Indels	21;	Gaps 4
Qy	26 LIRPLFLHRVOPGRRTLN-----LLRG--WREPAELPKLGAPS PGDKP DKLPEVPLSNYR 74			
	:: :: :: :: :	:: :: :: :	:: :: :: :	
Db	19 ITRFLKPFESTRRLNLSGSQUNVEQILLAGTSNLSONQGFPSNAPTP-----ETLKYNM 72			
Qy	75 DVQYFGEIGLGTGPONFTVAFDTGSSNLNWFSRCHFFSFVSDCWLHFRFDPKASSFSQANG 134			
	:: :: :: :: :	:: :: :: :	:: :: :: :	
Db	73 DAQTYGEIGLGTGPVQMFTVVYDGTSSNLWLDSTIHCSTSFTDIACLLHKYNGAKSSTYKNG 132			
Qy	135 TKEFALQYGTORVGDGLISEDTLTIGGIGKAGSTVIFGEALWEPSLVAFAHFEDGTLGLGPIL 194			
	:: :: :: :: :	:: :: :: :	:: :: :: :	
Db	133 DAQTYGEIGLGTGPVQMFTVVYDGTSSNLWLDSTIHCSTSFTDIACLLHKYNGAKSSTYKNG 192			
Qy	195 SVEGTRPPMDVLVEQGLLDKPKVFSESYLNRDDEPDDGELVYGGSDPAHYTIPPLTFYPTVY 254			
	:: :: :: :: :	:: :: :: :	:: :: :: :	
Db	193 SVDGTPPVFMOMMSQSKKVEQNFSYLYNRPNDTEPGELLGGTDPKXYTGDFNYVYVTR 252			
Qy	255 PAYQJHMERVKVGGLTCAKGAAILDGTSLIGPTEETRALHAAIGGIPPLAGEYI 314			
	:: :: :: :: :	:: :: :: :	:: :: :: :	
Db	253 QAYWQIHMDSMSIGSOLTLCKDGCNAIVDGTSLTGTGPAEVTRALQKAIGAQLPIQSEYM 312			
Qy	315 ILCSPITPKLAVSFVLLGFGWFLNLTADYVQTTRCLLSGFAQLDVPPAGPFWLIG 374			
	:: :: :: :: :	:: :: :: :	:: :: :: :	
Db	313 IDCKVPTPLETISRYNGKTYSLTSGEQYVULKESQGKTKICLUSGLMLEIIPPAGPLWLIG 372			
Qy	375 DVEFLGTYVAYEDRGDMKSSARVGLARA 401			
	:: :: :: :: :	:: :: :: :	:: :: :: :	
Db	373 DVFFIGYYTVFDR----ESNRVGFAKS 395			
<b>RESULT 5</b>				
CATD_HUMAN				
ID_CATD_HUMAN				
P07339; AC		STANDARD;	PRT;	412 AA.
DT 01-APR-1988 (Rel. 07, Created)				
DT 01-APR-1988 (Rel. 07, Last sequence update)				
DT 10-OCT-2003 (Rel. 42, Last annotation update)				
DE Cathepsin D precursor (IEC 3.4.23.5).				
GN CTSD.				
OS Homo sapiens (Human); Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OC OC				
NCBI_TaxID=9606; [1]				
RN RP SEQUENCE FROM N.A.				
RX MEDLINE=85270436; PubMed=192792;				
RA Faust, P.L., Kornfeld S., Chirgwin, J.M.;				
RT "Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive human breast cancer cells.";				
RL Proc. Natl. Acad. Sci. U.S.A. 82:4910-4914 (1985).				
RN [2]				
RN RP SEQUENCE FROM N.A.				
RX MEDLINE=87231068; PubMed=2588310;				
RA Westley, B.R., May F.B.B./				
RT "Cloning and sequence analysis of cDNA for human cathepsin D."				
RL Proc. Natl. Acad. Sci. U.S.A. 82:4910-4914 (1985).				
RN [3]				
RN RP SEQUENCE FROM N.A.				
RX MEDLINE=91299158; PubMed=2069717;				
RA Redeker, B., Heckendorf, B., Grossch H.W., Mersmann G., Hasilik A.;				
RT "Molecular organization of the human cathepsin D gene."				
RL DNA, Cell Biol. 10:423-431(1991).				
RN RP SEQUENCE FROM N.A.				
RC TISSUE-Kidney;				
RX MEDLINE=22388257; PubMed=12477932;				
RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,				
RA Klausner R.D., Collings F.S., Wagner L., Shanmen C.M., Schuler G.D.,				
RA Altenschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				



Page 6

65	EPSELLNNYLDAGXYGEIGITGPQCFTVWFDTGSNLWPSIHKCLLIACTWYHKYN	124	
124	PKSSSFQANGTRPAIQNTGRVDGILSED-----KLTIGGIKASAVTGEALWEPISLY	177	
125	SDFDSITYVKNGTSFSDIHGGSGSLDVTSPCKSPLIGGIKEKQPKGEATKPGVW	184	
178	FAFAHFDGLGLCPILSYEVPRPPMDVLFQEGHLDKPVFSFYLNRDPEPDGGELVLG	237	
185	FIAAKFDGLGMGPFIPISNKVLVDFNLMQKLVEKNLFSFYLNRDPTGTQPGG3BLMLGG	244	
238	SDPAHYXIPPLTFYPTVAYWQIHMERYVKGPGTLICARGCAAILDTGSLITGTPEELR	297	
245	TDSRYXHGELSYLNVTXRAYWCVMDOLEVGSSETLCKGGCEALVDTGSLLVPDVDEVK	304	
298	ALHAAIGGIPPLAGEYILLCSETPKLPAYSFLGGWVNLTADHYVIQTTRNGYRLC1SG	357	
305	ELOKAIGAVPLIQEYMPCERTKSSLPLTFKQGQNPLHPERYLKVSQAGR1TC1SG	364	
358	FQALDPPPAGPFWILGIVFLGTYVAEDRGDMKMSARGLAR1T	403	
365	FMDNDIPPSGPWILGIVFLGTYCTVFR----EYNRPFKASAT	406	

RESULT 7					
	STD MOUSE	CATD MOUSE	STANDARD;	PRT;	410 AA.
	P18242;				01-NOV-1990 (Rel. 16, Created)
					01-NOV-1990 (Rel. 16, Last sequence update)
					15-MAR-2004 (Rel. 43, Last annotation update)
					Cathepsin D precursor (EC 3.4.23.5).
					CTSD.
		Mus musculus (Mouse).			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
					NCBI_TAXID=10090; [1]
					SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=Brain; MEDLINE=91088345; PubMed=2263503;
					Diedrich J.P., Staskus K.A., Retzel E.F., Haase A.T.; "Nucleotide sequence of a cDNA encoding mouse cathepsin D."; Nucleic Acids Res. 18:7184-7184 (1990). [2]
					SEQUENCE FROM N.A. MEDLINE=90126544; PubMed=2374732;
					Grusby M.J., Mitchell S.C., Glimcher L.H.; "Molecular cloning of mouse cathepsin D."; Nucleic Acids Res. 18:4008-4010 (1990).

[3] SEQUENCE FROM N.A.  
 STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;  
 MEDLINE=22388257; PubMed=1247932;

HEITMAN M., Perschil A., Saftig P., von Figura K., Peters C.; "Mouse cathepsin D gene: molecular organization, characterization of the promoter, and chromosomal localization."; DNA Cell Biol. 13:419-427 (1994).

[4] SEQUENCE FROM N.A.  
 STRAIN=C57BL/6J; TISSUE=Brain, and Mammary gland;  
 MEDLINE=94280622; PubMed=8011168;

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Higgins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Uddin T.B., Yoshiaki S., Carnincos P., Prange C., Raha S.S., Loquellano N.N., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Mizrahi D.M., Scoderien F.J., Tsai Y., Gibbs P.A.

RA	Fahney J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakley R.W., Touchman J.W., Green D.B., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krywinski M.I., Skalska U., Smalius D.E., Scherzer A., Schein J.E., Jones S.J.M., Marr M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).	RT	-!- FUNCTION: Acid protease active in intracellular protein breakdown.	RT	-!- CATALYTIC ACTIVITY: Specificity similar to, but narrower than, that of pepsin A. Does not cleave the 4-Gln   -His 5 bond in insulin.	CC	-!- SUBUNIT: Consists of a light chain and a heavy chain.	CC	-!- SUBCELLULAR LOCATION: Lysosomal.	CC	-!- SIMILARITY: Belongs to peptidase family Al.	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	DR	EMBL; X53337; CAA37423.1; -.	DR	EMBL; X52886; CAA17067.1; -.	DR	EMBL; X52887; CAA17067.1; -.	DR	EMBL; X683378; CAA48453.1; JOINED.	DR	EMBL; X683379; CAA48453.1; JOINED.	DR	EMBL; X683380; CAA48453.1; JOINED.	DR	EMBL; X683381; CAA48453.1; JOINED.	DR	EMBL; X683382; CAA48453.1; JOINED.	DR	EMBL; X683383; CAA48453.1; JOINED.	DR	EMBL; BC05479B; AAH54758.1; -.	DR	EMBL; BC057931; AAH57931.1; -.	DR	Pfam; I42278; RHMSD.	DR	HSSP; P07339; ILYB.	DR	MERCPS; A01.009; -.	DR	MGD; MGI:885656; Ctsd.	DR	InterPro; IPR019699; Aspprotease_AS.	DR	InterPro; IPR009007; Pept_A_acid.	DR	InterPro; IPR01461; Peptidase_Ai.	DR	PFAM; PF00026; arg; 1.	DR	PRINTS; PR00792; PEPSIN.	DR	PROSITE; PS00141; ASP PROTEASE; 2.	KW	Hydrolase; Aspartyl peptidase; Glycoprotein; Lyosome; Zymogen; Signal.	FT	SIGNAL 1 20	FT	PROTEIN 21 64	FT	CHAIN 65 410	FT	ACT SITE 97 97	FT	ACT-SITE 293 293	FT	DISTRIFID 91 160	FT	DISTRIFID 110 117	FT	DISTRIFID 284 288	FT	DISTRIFID 327 364	FT	CARBOHYD 134 134	FT	CARBOHYD 261 261	SQ	SEQUENCE 410 AA; 44954 MW;	Query Match	44.3%; Score 992.5; DB 1; Length 410;	Best Local Similarity	47.7%; Pred. No. 1.e-72;	Matches	194; Conservative 67; Mismatches 125; Indels 21; Gaps 4;
QY	10 LLLPLNVEPSGATLIRIPLRVPQGPRTNLNRGHE-----PABLPKGAPSGFD 63	Db	7 LLLIGLU-ASSFAIRIPLRKFTSIRRTMTEVGGSVDELLKGPTIKYSMOSPKTT 64	QY	64 KPIFVPLNSRYDQYFGIGLGPQNPQTVAAPDTGSSLNLWPSRRCHFFSVPWLHFRFD 123	Db	65 EPYSELKKNLQDQYGDGIGTPQCPTVFDTGSSLNLWPSIHKFLDIAGWHHCKYN 124	QY	124 PKASSQFQANGTKTFPAIQYGTGRVGDGLLSEDKLTI- -----GGIGKASVTFGEALWP 174																																																																														

Db	125	SDKSSTTYVKNGTSFDIHYGSGSLSGLYSLQDTYSVPCKSDQSARGIKVEKQIFGEATKQP	184		FT	CARBOHYD	241	241	N-LINKED (GLCNAC. . . ) (POTENTIAL).	
Qy	175	SLVFAFAHEDGLIGLGPILSYEGRPPMDVLYEQGLIDKPKVFSEYFLNDRPEPDGGELV	234		SQ	SEQUENCE	390	AA;	42488 MW; 5B3BA1C3C4BD35 CRC64;	
Db	185	GIVFVAFKFDGLIGMGYPHISYANVLPPFDNLMOQLKLVDNIFSFYLNDRPEQGPGELEM	244		Query Match	43.2%	Score	967.5	DB 1; Length 390;	
Qy	235	LGGSDDPAHYIPPLTFPVPTVPAWQTHMERVKVGPGLTCAKGCAAIDTDGTSLITGTP	294		Best Local Similarity	48.3%	Pred.	No. 1.6e-3		
Db	245	LGQDTSKVHGELSYLNTRKAWQVNDQLEVNELLCKGCEATVDTGTSLLIVEPE	304		Matches	189; Conservative	58; Mismatches	125; Indels	19; Gaps 3;	
Qy	295	EIRALHAAGGIGPLLAGSYYLICSEIPKIPAVSFLIGQWENLTAHDYVIQTTRNGYRLC	354		Qy	26	LIRIPHLRVPQPERRTNLRLRW-----REPAELPKGAPSQDKRIFVPLSNYRDYQYF	79		
Db	305	EVRELQKAGAVPLQGYMIPSEKVKSSLPTVYLKCGRNVLHDPKXLYSQGRTIC	364		Db	1	VIRIPHLKFTSRTTNESEAAGKXKXLIAKGPISKVATGEPAVROGPipeLKNMNDQYY	60		
Qy	355	LSQFOALDVPAPPAGFPWNLGDVPLGTTAVFDRGDMKSAVGLARA	401		Qy	80	GBIGLGPBPQNPFTVAFDTGSSNLLWPSRCHFFSYSPCWLRHFRDPKAASSFOANGTKFAI	139		
Db	365	LSQFMGMIBPPPSGPLWNLGDVPTGTSYTVFDR---DNNRVYGFANA	407		Db	61	GEIGIGTGPQCPTVVEDTGSANLWPSIHKLLDIACTWHERKNSDKSSTVNRGTFDI	120		
					Qy	140	QYGTGRDVGILSEDKLTI-----GG1KGASVTFGEALWEPSPVUFAPAHFDGTLGLG	190		
					Db	121	HYSGSGUSGYSQDVTYSPVCPNCNPSSSRGGYTQRFQFGEAIKQPGVWFIIAKFGDGLGMA	180		
					Qy	191	FPILSVEGVYPMDVILVQEGLIDKPKVSFYLNRDPEPDGELVJGSDPAHYIPPLTFV	250		
					Db	181	YPRISYNVNLVPFDNLMQQLVDFKNNVFSFFLKNVTSKYRGSLMFH	240		
					Qy	251	PVTVPAYWQHMRVKGPGGILTCAKGCAAIDTDGTSLITGTPTEERALHAGGAPLLA	310		
					Db	241	NTVRQAYWQHMDQLDVGSSLTVCKGCEAIVDGTSLIVGPVEVRELQKAGAVPLIQ	300		
					Qy	311	GEYITLICSEIPLKPLAVSFLIGQWFLNLTADYVTCRNSYRLGSGFQALDVPPAGPF	370		
					Db	301	GEYMPICPKVSSLPLPVTVQGKDNTALSPEDYALVQSAETTVCLSGFMGMDIPPGGPL	360		
					Qy	371	WILGDYFLGLGTVAVFDRGDMKSSARYGLARA	401		
					Db	361	WILGDVFIGRYTTFVFRD---DQNRFVGLAEA	387		
<hr/>										
RESULT 8										
CATD_BOVIN	CATD_BOVIN	STANDARD;	PRT;	390 AA.		RESULT 9				
AC	P80209	Q9rs27;			ASPP_AEDAE					
DT	01-JUL-1993	(Rel. 26, Created)			ID	-ASPP_AEDAE	STANDARD;	PRT;	387 AA.	
DT	16-AUG-2001	(Rel. 40, Last sequence update)			AC	Q03168;				
DT	28-FEB-2003	(Rel. 41, Last annotation update)			DT	01-JUN-1994	(Rel. 29, Created)			
DE	Cathepsin D precursor	(EC 3.4.23.5).			DT	01-JUN-1994	(Rel. 29, Last sequence update)			
GN	Bos taurus (Bovine).				DB	28-FEB-2003	(Rel. 41, Last annotation update)			
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				DB	Lysosomal aspartic protease precursor (EC 3.4.23.-).				
OC	Mammalia; Butheria; Cetartiodactyla; Ruminantia; Bovidae;				OS	Aedes aegypti (Yellowfever mosquito).				
OC	Bovidae; Bovinae; Bos.				OC	Neoptera; Endopterygota; Culicoidea; Aedes.				
NCBI_TaxID	9913;				OC	Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.				
RN	[1]				OX	NCBI_TaxID-7159;				
RP	SEQUENCE OF 1-48.				RN	SEQUENCE FROM N.A., AND SEQUENCE OF 54-71.				
RC	TISSUE=Milk;				RX	MEDLINE=9302276; PubMed=8454061;				
RC	MEDLINE=93202276; PubMed=8454061;				RA	CHO W.L.; RAIKHEL A.S.; RAIKHEL T.S.				
RA	"Procathepsin D cannot autocinate to cathepsin D at acid pH.";				RA	Cho W.L., Raikhel A.S.; Raikhel T.S., Raikhel A.S.;				
RA	PEBS Lett. 319:54-58 (1993).				RA	"Purification and characterization of a lysosomal aspartic protease with cathepsin D activity from the mosquito.";				
RN	[12]				RA	Cho W.L., Raikhel A.S.; Raikhel T.S., Raikhel A.S.;				
RP	SEQUENCE OF 45-390, AND X-RAY CRYSTALLOGRAPHY (3 ANGSTROMS).				RT	"Cloning of cDNA for mosquito lysosomal aspartic protease. Sequence analysis of an insect lysosomal enzyme similar to cathepsins D and B."				
RC	TISSUE=Liver;				RT	RT				
RX	MEDLINE=93223670; PubMed=8467789;				RL	RL				
RA	Metcalf P., Fussak M.:				CC	FUNCTION: May degrade organelles involved in the biosynthesis and secretion of vitellogenin.				
RT	"Two crystal structures for cathepsin D: the lysosomal targeting signal and active site."				CC	-1- SUBUNIT: Homodimer.				
RL	RL				CC	-1- SUBCELLULAR LOCATION: Lysosomal.				
CC	CC				CC	-1- SIMILARITY: Belongs to peptidase family A1.				
CC	-1- PUNCTION: Acid protease active in intracellular protein breakdown.				CC	DR				
CC	that of pepsin A. Does not cleave the 4-Gln-1-His-5 bond in B chain of insulin.				CC	HSSP; P07399; 1MW.				
CC	-1- SUBUNIT: Consists of a light chain and a heavy chain.				CC	InterPro; IPR001469; ASPprotease_AS.				
CC	-1- SUBCELLULAR LOCATION: Lysosomal.				CC	InterPro; IPR003007; Pept_Acid.				
CC	-1- SIMILARITY: Belongs to peptidase family A1.				CC	DR; InterPro; IPR001461; Peptidase_A1.				
DR	DR				CC	PFam; PF00026; aspD_1.				
PRINTS	PRINTS; PR00792; PEPSIN.				CC	DR; InterPro; IPR00792; PEPSIN.				
PROSITE	PROSITE; PS00141; ASP PROTEASE; 2.				CC	DR; InterPro; IPR001461; ASP PROTEASE; 2.				
KW	Hydrolase; Asparagine peptidase; Glycoprotein; Lysosome; Zymogen.				CC	FT; ACT_CHAIN_1_44 ACTIVATION PEPTIDE.				
PROPEP	PROPEP 1_44 ACTIVATION PEPTIDE.				CC	FT; ACT_CHAIN_1_45 CATHEPSIN D.				
FT	FT				CC	-1- SUBCELLULAR LOCATION: Lysosomal.				
FT	ACT_SITE_77				CC	-1- SUBCELLULAR LOCATION: Homodimer.				
FT	ACT_SITE_273				CC	-1- SIMILARITY: Belongs to peptidase family A1.				
FT	DISULFID_71				CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Bioinformatics Institute and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial				
FT	DISULFID_90				CC	FT				
FT	DISULFID_264				CC	FT				
FT	DISULFID_307				CC	FT				
FT	DISULFID_114				CC	FT				

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CC	SEQUENCE OF 1-98.
CC	TISSUE=Spleen;
DR	EMBL: M95187; AAA29350.1; -.
DR	PIR; A45117; A5117.
DR	HSSP; P007197; 2REN.
MEROPS;	AOL_009; -.
DR	Siena2DPAGE; Q03166; -.
DR	Intero; IPR001969; Asprotease AS.
DR	InterPro; IPR00007; Pept_A_acid_
DR	InterPro; IPR001461; Peptidase_A1.
Pfam;	PF00026; asp; 1.
PRINTS;	PRO0792; PEPSIN.
PROSITE;	PS00141; ASP-PROTEASE; 2.
DR	Hydrolase; Aspartyl_Protease; Glycoprotein; Zymogen; Signal.
KW	SEQUENCE OF 104-345.
FT	FT SIGNAL 18
FT	FT PROPEP 19 REMOVED IN MATURE FORM.
FT	FT CHAIN 54 LYSOSOMAL ASPARTIC PROTEASE.
FT	FT ACT_SITE 86 BY SIMILARITY.
FT	FT ACT_SITE 272 BY SIMILARITY.
FT	FT DISUFDID 99 106 BY SIMILARITY.
FT	FT DISUFDID 263 267 BY SIMILARITY.
FT	FT DISUFDID 306 343 BY SIMILARITY.
FT	FT CARBOHYD 123 123 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE 387 AA; 41805 MW; 73A3C9E701E47FEC CRC64;
Query Match	43.1%; Score 964.5; DB 1; Length 387;
Best Local Similarity	48.5%; Pred. No. 2.8e-70;
Matches	192; Conservative 62; Mismatches 131; Indels 11; Gaps 5;
Qy	6 LLQPLIILPLUNVEPNSGATLIRIPHRVQGRTRNLRLGWREPAELPKLGAPS PGDKP 65
Db	2 LIKSIIALCVLAVL-SQADFVRVQLHKTESARQHFRNVTDEIKQURL-KINAVS--GP 55
Qy	66 IFVPLSNYRDYQYFGIGLGTSPQQNFTVAFTGSSNLWVPSRRCHEFFSTPCWLHFRDPK 125
Db	56 VPEPLSNYLDAQYYGATITGPQSKVQFDTGSNLWVPSKECSFTNAACLMEINKYNAK 115
Qy	126 ASSSFQANGTKFAIQYGTGRVGDGILSEDKELTIGKGASVIFGEALWEPPLVFAHFDG 185
Db	116 KSSTFEKNGTAFHIIQYGSSTSGYLSTDYGLGGDPEPDGELVIGGSDPAHYTP 245
Qy	186 ILGLGPILSVEGYRPMPDVLYEQLGKLDKEVFSFYLNRLDPEPDGELVIGGSDPAHYTP 245
Db	176 ILGLGYSSISYSDGVIVPVYNNQGLIDAPVFSFLNRDSAAEGEIIFGGSDSNKYTG 235
Qy	246 PLTFVPTVTDAYQWTHMERYTKVGPGSLTLCAKGCAAILDTGTSLITGPTBEIRALHAIGG 305
Db	236 DFTYLSVDRKAYWQFMDSYKVG-DTEFCNGCEAATDTSILAGPVSVTAINKAGG 294
Qy	306 IPLLAGEYIILCSEIPKLPAYSFLGGWWMNLTAHDYVITTRNGVRLLCGFQALDVP 365
Db	295 TPIMNGEYMMYDCSL1PKLPKISFLVLLGKSPDFLEGADYVVRVAQMGKTCIISGFENGIDIP 354
Qy	366 PAGPPWILDGVFLGYVAVFDRGDMKGSARVGLARA 401
Db	355 PNGPLWILDGVFLGYTYTFDMG---NDRVGPATA 386
RESULT 10	Query Match 42.2%; Score 944; DB 1; Length 345;
CATD_PIG	Best Local Similarity 52.7%; Pred. No. 1.e-68;
ID_CATD_PIG	Matches 183; Conservative 48; Mismatches 102; Indels 14; Gaps 4;
AC	65 PIFVPLSNYRDVQYFGIGLGTSPQQNFTVAFTGSSNLWVPSERCHFFSVPCWLHFRDP 124
P00755;	2 PIPEVLRKMYMDAQYYGEIGIGTPOQCFTVFDTGSNLWVPSTHCKLIDIACTIHAKTNS 61
DT	21-JUL-1996 (Rel. 01, Created)
DT	01-NOV-1990 (Rel. 16, Last sequence update)
DE	Cathepsin D (EC 3.4.23.5).
GN	125 KASSSFQANGTKFAIQYGTGRVGDILSEDKELT--TGGIGKASVIFGEALWEP 174
CTSD.	62 GKSSSFQANGTKFAIQYGTGRVGDILSEDKELT--TGGIGKASVIFGEALWEP 121
OS	175 SILVRAFAAHFDGILGLGFPLISVYGRVPPMDVLEQGLDKKPVFSYLNRDPEPDGGBLV 234
Eukaryota; Chordata; Craniata; Vertebrata; Buteleostomi;	NCBI_TaxID=9823;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sub;	NCBI_TaxID=9823;
122 GLTRTAAKPFDGILGMAYPRISVNNVVPYEDNLMQKLVDKD1F5FYLNRDGPQGPQG3ELM 181	

QY	235	LGGSDDPAHYIPPLTFVPTVTPAYNQHMMERVKVPGGLTCAKGCAAIIIDGTSLITGDPPE	294	KW Hydrodrolase; Aspartyl protease; Glycoprotein; Zymogen;
Ddb	182	LGGSDDKYKSGSLDHNTRKAYQIHMNVQAVAGSLSLTLKGGCAAVDTGTSLTVGQDE	241	KW Lysosome; Disease mutation.
QY	295	EIRALHAAGCIGIPLLAGETILLCSELPKLAIVSFLGGTWFNLTHHDYIQTTRNGVRLLC	354	FT ACT_NER <1 1 39 ACTIVATION PEPTIDE.
Ddb	242	EYRELGKIAIGAVPLIQEYMLPCYPSLSDPVTVNLGGKCYKLSSENTLVKSQAGQTTC	301	FT PROTEP <1 1 39 CATHESPIN D.
QY	355	LSGFQFQALDVPPPAGEPFWILGDVFGLRNYVAVFDRGDMKSAVGRGLARA 401	401	FT ACT_SITE 4.0 >365 BY SIMILARITY.
Ddb	302	LSGFNGMDIPPGPLWILGDVFGLRNYVAVFDRGDMKSAVGRGLARA 344	344	FT ACT_SITE 7.2 268 BY SIMILARITY.
QY	365	FT DISULFID 66 135 BY SIMILARITY.		
Ddb	365	FT DISULFID 85 92 BY SIMILARITY.		
GN	CTSD	FT DISULFID 259 263 BY SIMILARITY.		
QY	365	FT DISULFID 302 339 BY SIMILARITY.		
Ddb	365	FT VARIANT 268 268 D -> N (IN CONCL; INACTIVE).		
SQ	365 AA;	39814 MW;	7667BFE5BC45B9CB CRC64;	
		Query Match 41.2%; Score 922.5; DB 1; Length 365;		
		Best Local Similarity 47.7%; Pred. No. 6.2e-67;		
		Matches 175; Conservative 61; Mismatches 110; Indels 21; Gaps 4;		
QY	31	LHRVQPGFRRTLNLLRGWREPAE-----LPKLGAPSPGDK--PIFVPLSNRYDQYQFGE 81	81	
Db	1	LHKFETSNRRTMSEAMG--PVEHLIAKGPIISKYATREPRAVQGPPELLTNMDAOYQGE 57	57	
QY	82	IQLGTRPQNFTVAFDTGSSNLMWPSBRCHFSPVPUHEDPKASSSFQANGTKPAIQY 141	141	
Db	58	IGIGTTPQCFTVVFDTGSANLMWPSIHKULDIACTWVHHCKNSDSSTSYYRNGTSDIHY 117	117	
QY	142	GTGRVGQGILSSDQLLT-----GGIKGASAVIFVGEALWEPSSLVFAFADGILGLGFP 192	192	
Db	118	GSGSISQSYISQDPTVSPCNDSSSSSGCVTYHQQTFTAIIKOPGVFIAAKDGLGMAPY 177	177	
QY	193	ILSVEGYRPMDVLVSGQGLDKEPKVPSFLYNDPEPDGGELVLGGSDDPAHYIPTPLTFVFP 252	252	
Db	178	RISVNNVLPVFDNLNLQKLVKQNVISFFLARDPKAOQGEELMLGGTDSKTYRGSLSYHN 237	237	
QY	253	TVPATQWHMRVKVGRGLTCAKGCAAIIIDGTSLITGPTTEEIRALAAIGGIPPLAGE 312	312	
Db	238	TRQAYQWHMDQDVSLLTICKGGCEAIVDTGTSLMVGPVDDEVRLHKAIGAVPIQGE 297	297	
QY	313	XIILCSIEPKUPAVSFILLGGYWENLTAHDYVQTTRNGVRLCLSGQALDYPAPPGPFWI 372	372	
Db	298	YMPICPERVSSLRQVTEKLKGDDYTSPEPDYFLKVSQAGTYFLGSMGMDPPG3QPLWI 357	357	
				RESULT 1.2
				CATE_MOUSE
				ID_CATE_MOUSE STANDARD; PRT; 397 AA.
				AC_P70269; 035647;
				DT 01-NOV-1997 (Rel. 35, Created)
				DT 15-MAR-2004 (Rel. 43, Last annotation update)
				DR Cathepsin B precursor (IEC 3.4.23-34).
				DR CTSE.
				OS Mus musculus (Mouse).
				OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
				OC Mammalia; Butiorrhiza; Rodentia; Sciurognathi; Murinae; Mus.
				OX NCBI_TaxID:10909;
				RN SEQUENCE FROM N.A.
				RP STRAIN=BALB/C; TISSUE=Spleen;
				RC MEDLINE=97324100; PubMed=9180269;
				RA Ratnelli P.J.; Lees W.E.; Kay J.;
				RT "Cloning, expression and characterisation of murine procathepsin E.;"
				RN [2]
				RP Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
				RC SPTRAIN=129/SvJ;
				RA Ratnelli P.J.; Roth W.; Duesing J.; Kay J.; Peters C.
				DR HSSP; P07339; IIBB.
				DR MEROPS; A01_009; Asprotease_AS.
				DR InterPro; IPR001569; Pept_A acid.
				DR InterPro; IPR001661; Peptidase_A1.
				DR pfam; PF00026; app; 1.
				DR PROSITE; PS00141; ASP PROTEASE; 2.
				DR PRINTS; PR00122; PEPSIN.

[3]	SEQUENCE FROM N.A.	Qy	60 SPGDKPLFVPLSNYRDVQYFEGIIGSTPPONETVAFDTGSSNLWBSRRCHEFFSPCWHL 119
RT	STRAIN=FBN; TISSUE=Mammary gland;	Db	61 CNVYSSSYNEPLINYLMEMYFOTISCTPQANFTVFDTGSSNLWIVSVIC-TSPACKAH 118
RC	MEDLINE=22388257; PubMed=12477932;	Qy	62 HRFDPKASSSFQANGTKFAILOYGTGRDGILSEDKLUTTIGGKGASATVFGRALWEPSLVFA 179
RX	Straubinger R.L., Peingold B.S., Grouse L.H., Derge J.G., Schuler G.D.,	Db	120 HRFDPKASSSFQANGTKFAILOYGTGRDGILSEDKLUTTIGGKGASATVFGRALWEPSLVFA 179
RA	Klauserer R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,	Qy	119 PVFHPSQSDDTVEGNHFSILOYGTSLTGAGDVSVEGLTVDQGQFGEVKPEQQTGV 178
RA	Altschul S.F., Zeeberg B., Buerk K.H., Max S.I., Wang J., Hsieh F.,	Db	180 FAHFDTLGIIGEPILLSPVLSVCEGRPPMDVTECQDLSKPIVNRNDEPDCGELLUGGSD 239
RA	Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,	Qy	179 NAEFDGILGLGICPSLAAGGTPVFNFMMAQLNVALPMFSTYLSSPRQGGSSELTFGGYD 238
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	Db	240 PAHYEPLTFPVPTVPAWQWIMEVKVGGLTARGCAAILDGTSLITGPBIRAL 299
RA	Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schuetz T.E.,	Qy	239 PSHFSGSLANVNPVTKOAYWQTAQDQVGDYVMESEGCQAVTGTSLITGPBIRAL 298
RA	Brownstein M.J., Ustdin T.B., Toshiyuki S., Carninci P., Prange C.,	Db	300 HAAGGCIPLLAGETTILCSEPKLDAVSFLLGQWENLTAHDYVYQTTTRNGVRLLSGFQ 359
RA	Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mulahay S.J.,	Qy	299 QEAIGATP-IDGEYAWDCATLDTMNTFLINEYTYLNPTDYLVDGMQFFGSGFQ 357
RA	Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,	Db	360 ALDVPBPAGPEWILGDFVLTGTYVAFDRGDMKSSARVGLARA 401
RA	Richards S., Worley K.C., Hale S., Garcia A.N., Gay L.J., Rulyk S.W.,	Qy	358 GLDIPPPAGPLWILDGVTRQFYSVDFRG---NNQVGLAPA 395
RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,	Db	
RA	Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,		
RA	Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,		
RA	Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.,		
RT	"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
CC	-!- CATALYTIC ACTIVITY: Similar to its intracellular location and distribution in lymphoid associated tissue, it may have a role in immune function.		
CC	-!- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader specificity.		
CC	-!- SUBUNIT: Homodimer; disulfide-linked (By similarity).		
CC	-!- SIMILARITY: Belongs to peptidase family Al.		
CC			
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CC			
DR	EMBL: Y97399; CAA66056.1; --.	ID	CATHE HUMAN
DR	EMBL: Y10928; CAA71859.1; --.	CATE_HUMAN	STANDARD:
DR	EMBL: BC005432; AAH05432.1; --.	P1491;	PRT;
DR	HSSP: P00794; 4CMS.	DT	01-1990 (Rel. 13, Created)
DR	PRINTS: PR00792; PEPSIN.	DT	01-JUN-1990 (Rel. 13, Last sequence update)
DR	MEROPS: AOL:010; --.	DB	10-OCT-2003 (Rel. 42, Last annotation update)
DR	MGD: MGI:107361; Ctsee.	CTSF_E	Precursor (EC 3.4.23.34).
DR	InterPro: IPR001969; Aspartate AS.	GN	Homo sapiens (Human).
DR	InterPro: IPR009007; Pept. A acid.	OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
DR	InterPro: IPR001461; Peptidase_A1.	OC	
DR	pfam: PF00026; asp_1.	NCB_	
DR	PRINTS: PR00794; 4CMS.	NCB_	
DR	PROSITE: PS00141; ASP PROTEASE; 2.	TAXID=9606;	
RW	Hydrolase; Aspartyl protease; Glycoprotein; Zymogen; Signal.	RN	SEQUENCE FROM N.A.
FT	SIGNAL 1 18 BY SIMILARITY.	RN	SEQUENCE FROM N.A.
FT	PROPEP 19 59 ACTIVATION PEPTIDE (BY SIMILARITY).	RN	SEQUENCE FROM N.A.
FT	CHAIN 60 397 CATHESIN_E.	RN	SEQUENCE FROM N.A.
FT	ACT SITE 97 97 BY SIMILARITY.	RN	SEQUENCE FROM N.A.
FT	ACT SITE 282 282 BY SIMILARITY.	RN	SEQUENCE FROM N.A.
FT	DISULFID 61 61 INTERCHAIN (PROBABLE).	RN	"Human procathepsin E"; Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
FT	DISULFID 110 115 BY SIMILARITY.	RN	
FT	DISULFID 273 277 BY SIMILARITY.	RN	
FT	CARBOHYD 91 91 N-LINKED (GLCNAC. . . ) (POTENTIAL).	RN	
FT	CARBOHYD 323 323 N-LINKED (GLCNAC. . . ) (POTENTIAL).	RN	
FT	CONFLICT 297 297 H -> Q (IN REF. 2).	RN	
SQ	SEQUENCE 397 AA; 42932 MW; 8393FFE3AB36105 CRC64;	RX	
Query Match	Score 39.2%; Best Local Similarity 45.5%; Matches 183; Conservative 67; Mismatches 138; Indels 14; Gaps 6;	RA	Strasberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D., Altchul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Casavant T.L., Brownstein M.J., Ustdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loqueland N.A., Peters G.J., Abramson R.D., Mullany S.J., Bosak S.A., McEwan P.J., McErath K.J.A., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Garcia A.M., Gay L.J., Hulyk S.W.,
Qy	5 PLLQQPULLPLNVPSPGTLIRIPLHRYQPGRET---NLRGWR-EPAEIPKLGAP 59	RA	
Db	3 PLL-VLLILLILDIQAQGALHRYPLRHSQSLRKLRQAGQSLSEFWRSHNLDTRLSES 60	RA	

RA	Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimeswood J., Schmitz J.J., Myers R.M., Rodriguez Y.S.N., Krzywinski M.I., Skalska U., Smailus D.B., Schnarch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences." Proc. Natl. Acad. Sci. U.S.A. 99:1689-16903 (2002). [5]	Query Match 38 8%; Score 869; DB 1; Length 396; Best Local Similarity 45 1%; Pred. NO. 1.4e-62; Mismatches 136; Indels 12; Gaps 5; Matches: 179; Conservative 70; Substitutions 10; Insertions 1; Deletions 1.
RA	SEQUENCE OF 54-68; PubMed=334440; RX MEDLINE=9041267; PubMed=334440; RA Athauda S.B.P., Matsuzaki O., Kgeyama T., Takahashi K.; "Structural evidence for two isoformic forms and the carbohydrate attachment site of human gastric cathepsin E." Biochem. Biophys. Res. Commun. 168:878-885 (1990).	Query Match 10 10%; Score 510; DB 1; Length 124; Best Local Similarity 45 1%; Pred. NO. 1.4e-62; Mismatches 136; Indels 12; Gaps 5; Matches: 179; Conservative 70; Substitutions 10; Insertions 1; Deletions 1.
RN	"!- FUNCTION: Due to its intracellular location and distribution in lymphoid tissue, it may have a role in immune function. -!- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader specificity." CC -!- SIMILARITY: Belongs to peptidase family A1.	Query Match 65 6%; Score 510; DB 1; Length 124; Best Local Similarity 45 1%; Pred. NO. 1.4e-62; Mismatches 136; Indels 12; Gaps 5; Matches: 179; Conservative 70; Substitutions 10; Insertions 1; Deletions 1.
CC	DR EMBL: M84424; AAH4413; AAH52300.1; JOINED. DR EMBL: M84417; AAH52300.1; JOINED. DR EMBL: M84418; AAH52300.1; JOINED. DR EMBL: M84419; AAH52300.1; JOINED. DR EMBL: M84420; AAH52300.1; JOINED. DR EMBL: M84421; AAH52300.1; JOINED. DR EMBL: M84422; AAH52300.1; JOINED. DR EMBL: J05046; AAH52300.1; JOINED. DR EMBL: AJ250717; CABB2850.1; -. DR EMBL: BC042537; AAHA42537.1; -. DR PIR: A42038; A34401. DR PDB: 1LCG; 17-ASR-02. DR MEROPS: A01_010; -. DR Genew; HGNC: 2530; CTSE. DR MIM; 116890; -. GO: GO:0007586; P:digestion; TAS. DR Interpro; IPR001969; Asparteate-AS. DR Interpro; IPR005007; Pept_A_acid. DR Pfam; PF00026; asp_1. DR PRINTS; PR00792; PEPSIN. DR PROSITE; PS00141; ASP PROTEASE; 2. DR KW Hydrolyse; Aspartyl protease; Glycoprotein; Zymogen; Signal; Polymorphism; Pyrolyzed carboxylic acid; 3D-structure. KW SIGNAL 1 17 ACTIVATION PEPTIDE. FT PROPEP 18 53 CATEPHESIN E. FT CHAIN 54 396 PYRROLIDONE CARBOXYLIC ACID. FT MOD RES 18 18 BY SIMILARITY. FT ACT SITE 96 96 BY SIMILARITY. FT ACT SITE 281 281 BY SIMILARITY. FT DISULFID 60 60 INVERCHIN (PROBABLE). FT DISULFID 109 114 BY SIMILARITY. FT DISULFID 272 276 BY SIMILARITY. FT DISULFID 314 351 BY SIMILARITY. FT CARBOHYD 90 90 N-LINKED (GLCNAC. .). FT CARBOHYD 220 220 O-LINKED (POTENTIAL). FT CARBOHYD 333 333 O-LINKED (POTENTIAL). FT VARIANT 324 324 T -> I. (in dbSNP: 6503). /FTId=VBR_014572. SQ SEQUENCE 396 AA; 42793 MW; 40B643C5FB01521E CRC64;	Query Match 125 KASSSFQANGTKFAIYQGTGRVGDILSEDKLTIIGKAVGASVIFGBALWEPSLVFAHFD 184; DB 123 SQSSRISQPQGSFSQYGISSLSGIGADAVSVQELTVYQQFGEVSVTQGOTVDAEF 182; DB 185 GILGLGEPILSVEGVRPPMDVLYVEQGLDKPKFVSTYLNRDPEEPGGELVLGG3SDPAHYI 244; DB 183 GILGLGCPSPSLAVGGTTPVFNMMAGQLVLPMFSTYMSNPPEGGASESELFGGTDHSHFS 242; DB 245 PPLTFIPVTPVAYQWTHMERYVKGVGLTCAKGCAILDGTLGTTGPEERIAHALAAG 304; DB 243 GSINWNPVTKQAYWQALDNQVOGTVMFESEGCCQAIVDGTGTSLITGSPDKIKQQLONAIG 302; DB 305 GIPLLAGETYLCSSEIPKGIAVPSFLGGWVNLTADHYVITQTRNGVRLLGSGFGLDVP 364; DB 303 AAP-VDEGEAYECAANLVNMVDVTFTINGVPTLSSATYILDFTDVGMQFCSSGFQGLDIIH 361; DB 365 PPAGPFWILGDFVFLGTYVAYEDRGDMKSSARVGLARA 401; DB 362 PPAGPLWILGDFVIROFYSVDRG---NNRVLGLAPA 394
		RESULT 14 CAT_E RAT STANDARD; PRT: 398 AA. ID_CATE_RAT ID_P16228; 083701; AC DT 01-APR-1990 (Rel. 14, Created) DT 15-TUL-1998 (Rel. 36, Last sequence update) DT 28-FEB-2003 (Rel. 41, Last annotation update) DE Catepsin E precursor (BC 3.4.23.34). CTSB. GN Rattus norvegicus (Rat) OS Rattus norvegicus (Rat) OC Bokaryota; Metazoa; Chordata; Craniata; Vertebrata; Butteleostomi; OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. RN [1] NCBI_TaxID=10116; RN SEQUENCE FROM N.A. RP RC TISSUE=Spleen; RX MEDLINE=96104755; PubMed=7574663; RX RT "Isolation and sequencing of two cDNA clones encoding rat spleen RT cathepsin E and analysis of the activation of purified procathepsin E." B. RL Arc. Biochem. Biophys. 322:103-111(1995). RN [2] RSEQUENCE OF 59-110. RP MEDLINE=90147750; PubMed=2105725; RX RA Yonezawa S., Takahashi T., Ichinose M., Miki K., Tanaka J., Gasa S.; RT "Structural studies of rat cathepsin E: amino-terminal structure and carbohydrate units of mature enzyme." Biochem. Biophys. Res. Commun. 166:1032-1039(1990); RL CC -!- FUNCTION: Due to its intracellular location and distribution in CC lymphoid associated tissue, it may have a role in immune function. CC -!- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader CC specificity. CC -!- SUBUNIT: Homodimer; disulfide-linked. CC -!- ALTERNATIVE PRODUCTS: CC Event=Alternative splicing; Named isoforms=2; CC Name=long; IsoId=PI6228-1; Sequence=Displayed; CC Name=Short; Name=Short;

CC	-1- SIMILARITY: Belongs to peptidase family Al.	Db	364 PPAGPDLWIGDVTFIRKFYSVFDRG---NNQVGLAPA 396
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to licensee@isb-sib.ch).	RESULT 15:	
CC	DR EMBL; D38104; BAA08128.1; - .	CATE_RAB <sup>T</sup>	STANDARD, PRT; 396 AA.
CC	DR PIR; A34657; A34657. .	ID CATE_RABIT	PRT; 396 AA.
CC	DR HSSP; P00794; 4CM5. .	AC P43159;	Rel. 32, Created
CC	DR InterPro; IPR001969; Asprotease_AS.	DT 01-NOV-1995 (Rel. 32, Last sequence update)	
CC	DR InterPro; IPR009007; Pept_A_acid.	DT 01-NOV-1995 (Rel. 32, Last sequence update)	
CC	DR Pfam; PF00026; asp; 1.	DT 28-FEB-2003 (Rel. 41, Last annotation update)	
CC	PRINTS; PR00792; PEPSIN.	DB Cathepsin_E Precursor (EC 3.4.23.34).	
CC	DR PROSITE; PS00141; ASP-PROTEASE_2.	GN	
CC	DR Hydrolase; Aspartyl_protease; Glycoprotein; Zymogen; Signal;	OS Oryctolagus cuniculus (Rabbit).	
CC	DR KW Alternative_splicing; Pyrrolidine_carboxylic_acid.	OC Mammalia: Eutheria; Lagomorpha; Leporidae; Oryctolagidae; Oryctolagidae.	
CC	FT SIGNAL 1 19	RA Kagiyama T.; [1]	
CC	FT PROSP 20 58	RA "Rabbit procathepsin E and cathepsin E. Nucleotide sequence of cDNA, hydrolytic specificity for biologically active peptides and gene expression during development.".	
CC	FT CHAIN 59 398	RLJ Eur J. Biochem. 216:717-728(1993).	
CC	FT MOD_RES 20 20	CC -1- FUNCTION: Due to its intracellular location and distribution in lymphoid associated tissue, it may have a role in immune function.	
CC	FT ACT_SITE 98 98	CC -1- CATALYTIC ACTIVITY: Similar to cathepsin D, but slightly broader specificity.	
CC	FT DISULFID 62 62	CC -1- SUBUNIT: Homodimer; disulfide-linked (By similarity).	
CC	FT DISULFID 111 116	CC -1- SIMILARITY: Belongs to peptidase family Al.	
CC	FT DISULFID 274 278	CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a> or send an email to licensee@isb-sib.ch).	
CC	FT CARBOHYD 92 92	CC DR PIR; S36865; S36865.	
CC	FT VARSPLIC 312 344	CC DR HSSP; P00794; 4CM5.	
CC	FT VARIANT 114 114	CC DR MEROPS; A01.010; -.	
CC	FT CONFLICT 79 79	CC DR InterPro; IPR009007; Pept_A_acid.	
CC	FT SEQUENCE 83 84	CC DR InterPro; IPR001461; Peptidase_Al.	
SQ	SEQUENCE 398 AA; 43021 MW; 25F123E6/C46B5F CRC64;	PFam; PF00026; asp; 1.	
Qy	Query Match	PRINTS; PS00141; ASP-PROTEASE; 1.	
Qy	Best Local Similarity 38.7%; Score 867; DB 1; Length 398;	KW Hydrolase; Aspartyl_Protease; Glycoprotein; Zymogen; Signal;	
Qy	Matches 180; Conservative 68; Mismatches 137; Indels 12; Gaps 5;	KW Pyrrolidone carboxylic acid.	
Qy	10 LLLLPLPLNVEPGATLIRIPLHRYQPGRRL---NLRLGWR-EPAEPLPKLGAPS PGDK 64	FT SIGNAL 1 17	POTENTIAL.
Db	7 LLLLPLPLNLDLAQQGVLHRYPLRREQLSLRKLAQGQLSDFWRSNHLDTFESESCNV DK 66	FT PROSP 18 53	ACTIVATION PEPTIDE (BY SIMILARITY).
Qy	65 PIFVPLISNPYDQVYFELIGLCTPPONETVADTGSSNLWPSRSHFESYPCWLHFRFPD 124	FT CHAIN 54 396	CATHPSIN E.
Db	67 GINEPLINYLDMEYGTGVSGPSQNFTVTFDTGSSNLWPSVYC-TSPACKAHPVFP 124	FT MOD_RES 18 18	PYRROLIDONE CARBOXYLIC ACID
Qy	125 KASSFOQANGTKFAFOYGTGRDGTLSKEDKLITGIGTKGASVIFGRALWPEPSLYFAFAHD 184	FT DISULFID 314 351	(BY SIMILARITY).
Db	125 SQSSTYMEVNRHSFQYGTGSSLTGTGIAODPSVSEGTVFEGQFGEVSKEFGQT PVNAED 184	FT SEQUENCE 396 AA; 42679 MW; E5D84F248DC760A4 CRC34;	BY SIMILARITY.
Qy	185 GILGLGPFLSVEGYRPMPDMVLEQCLDPKFVFSYLNRDPEPDGGELVLGSSDPAHYI 244	FT ACT SITE 281	BY SIMILARITY.
Db	185 GILGLGPFLSVEGYRPMPDMVLEQCLDPKFVFSYLNRDPEPDGGELVLGSSDPAHYI 244	FT DISULFID 60	INTERCHAIN (PROBABLE).
Qy	125 KASSFOQANGTKFAFOYGTGRDGTLSKEDKLITGIGTKGASVIFGRALWPEPSLYFAFAHD 184	FT DISULFID 109	BY SIMILARITY.
Db	125 SQSSTYMEVNRHSFQYGTGSSLTGTGIAODPSVSEGTVFEGQFGEVSKEFGQT PVNAED 184	FT DISULFID 272	BY SIMILARITY.
Qy	245 PPLITVPVTPAYWQHMRVKGPFLTLAKGCAALDTSLLTGTSLTGTPEIRAHAAIG 304	FT DISULFID 314 351	BY SIMILARITY.
Db	245 GSLNWTPVTPKQWQIALDQIQVGDVTMVFSEGCOAVIDGTSLLTGPKKIKQLOQEA G 304	FT ACT SITE 96	BY SIMILARITY.
Qy	305 GIPLLAGETYIILCSEIPKLPDAVSEFLGGVFNLTADYTTQTRTRNGVRVLCSGFQALDYP 364	FT PROSP 18 53	ACTIVATION PEPTIDE (BY SIMILARITY).
Db	305 ATP-MGEYAVDCATINMMMPNVTFLINGVYTLSTAYLPLDVGMQFCGSQFQGLDDQ 363	FT CHAIN 54 396	BY SIMILARITY.
Qy	365 PPAGPFWLIDVFLGTYVAFDRGDMKSARVGLARA 401	FT MOD_RES 18 18	BY SIMILARITY.
Qy	9 PLUPLPLNVEPGATLIRIPLHRYQPGRRL---NLRLGWR-EPAEPLPKLGAPS PG 62	FT DISULFID 114 276	BY SIMILARITY.
Db	5 PLUPLPLNVEPGATLIRIPLHRYQPGRRL---NLRLGWR-EPAEPLPKLGAPS PG 62	FT ACT SITE 60	BY SIMILARITY.

QY 63 DKPIFVPLSNRYDQYFGEIGLGPQQNPTVAFTGSSNLWVPSRRCHFSSVPCWLHHRF 122  
 Db 63 EOSANEPLINYLDMEYWPRTSISGSPPONETVIEDTWSNLWVPBVYC--TSPACQMHQF 120  
 QY 123 DPKAASSFQANGTKPAIQXETGRDGLLSDDKLUTGGIKGASVIFGEALMESPSSVAFAH 182  
 Db 121 RPSQSNTSYEVGTTPSIAYTGSLTGIDQSVQGLTVGQQFGESEKPGOTVNAE 180  
 QY 183 FDGILGLGFPLSVEGVRPMPMDVLYEQGLDKPKYFSFYLNRDPEBDGGBLVLGSDPAH 242  
 Db 181 FDGILGLGYPSLAAAGGTVPFDNMMAONLYSLPMFSVWNNSNPBEGSGSBLTFCGYDSHH 240  
 QY 243 YIPPLTFVPTVPAWQIHEMERVKCQGLTCAKGCAAIDTGTSLITGPTEIRALHRA 302  
 Db 241 FSGSINNWVPTVKQGMQIADEIQVGGSPMFPCPECQAIVDTGSLITPSDKLKIQLQRA 300  
 QY 303 IGGIPPLAGEYLILCSEIPKLPAVNSFLGGYWFLNLTADYVIQTRNGVRLCLSGFOALD 362  
 Db 301 IGATP-MDGBAYAVECENTNIMPDTFVINGSVPTISATAYTLPDFDGMQFCGSSGRQGELD 359  
 QY 363 VPPPAGPFWLIGDVFLGTAVAFDRGDMKGSARVGLARA 401  
 Db 360 IQPPAGPLWILGDVFIRQFYSVFDRG---SNRVGLAPA 394

Search completed: June 2, 2004, 20:19:35  
 Job time : 18.3371 secs

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## OM protein - protein search, using sw model

Run on: June 2, 2004, 20:14:10 ; Search time 28.59 seconds  
(without alignments)  
1413.039 Million cell updates/sec

Title: US-09-700-770-8

Perfect score: 2238

Sequence: 1 MSPPPLQPLLLPLPLNVE.....ARTRGADLGWGTAAQOFG 420

Scoring table: BLOSUM62

GapOp 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR\_78:\*

1: Pir1:\*

2: Pir2:\*

3: Pir3:\*

4: Pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1030	46.0	398	2 151185	cathepsin D (EC 3.4.2)
2	1005	45.4	412	1 KHRUD	cathepsin D (EC 3.4.2)
3	1005	44.9	407	1 KHRUD	cathepsin D (EC 3.4.2)
4	992.5	44.3	410	1 KMSD	cathepsin D (EC 3.4.2)
5	992.5	43.1	387	2 A45117	aspartic proteinases
6	954.5	42.6	344	1 KHPGD	cathepsin D (EC 3.4.2)
7	905.5	40.5	444	2 T24204	hypothetical prote
8	869	38.8	396	2 S64401	cathepsin E (EC 3.4.2)
9	867	38.7	398	2 S66465	cathepsin E (EC 3.4.2)
10	848.5	37.9	396	2 S36865	cathepsin E (EC 3.4.2)
11	830	37.1	508	2 S66967	cathepsin E (EC 3.4.2)
12	808.5	36.1	401	1 REMSS	aspartic proteinases
13	806.5	36.0	391	2 A43356	renin (EC 3.4.23.1)
14	804	35.9	509	2 S66516	cathepsin E (EC 3.4.2)
15	803.5	35.9	442	2 JC5077	aspartic proteinases
16	797	35.6	402	1 REMSK	renin (EC 3.4.23.1)
17	789.5	35.3	365	2 S66466	cathepsin E (EC 3.4.23.1)
18	783	35.0	400	2 I47099	renin (EC 3.4.23.1)
19	779	34.8	402	1 RERTK	renin (EC 3.4.23.1)
20	779	34.8	406	1 REHUK	renin (EC 3.4.23.1)
21	778.5	34.8	474	2 T12049	cyprosin (EC 3.4.2)
22	778	34.8	513	2 T11686	aspartic proteinases
23	774	34.6	506	2 T07915	probable aspartic
24	774	34.6	508	2 DB8056	aspartic proteinases
25	773.5	34.6	496	2 JS0732	aspartic endopeptidase
26	769.5	34.4	513	2 S19682	pepsin A (EC 3.4.2)
27	767.5	34.3	388	2 F86253	hypothetical prote
28	766.5	34.2	506	2 PEMQAR	pepsin A (EC 3.4.2)

## RESULT 1

151185

cathepsin D (EC 3.4.23.5) precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 04-Sep-1997 #sequence\_revision 04-Sep-1997 #text\_change 22-Jun-1999

C;Accession: I51185

R;Retzek, H.; Steyer, B.; Sanders, E.J.; Nimpf, J.; Schneider, W.J.

A;Title: Molecular cloning and functional characterization of chicken cathepsin D, a

A;Reference number: I51185; PMID:93039672; PMID:1418623

A;Accession: I51185

A;Molecule type: mRNA

A;Residues: 1-398 &lt;RET&gt;

A;Cross-references: GB:S49650; NID:9259834; PIDN:AA24157.1; PID:g259835

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase

## Query Match 1 MSPPPLQPLLLPLNVEPSGATLIRPLHLRVQGPRTNLRLGRWREPAELPKLGA--

Best Local Similarity 46.0% Score 1030; DB 2; Length 398;

Matches: 208; Conservative 57; Mis matches 115; Indels 36; Gaps 7;

QY |:|:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||

## RESULT 2

GTSLSITGTPTBEIRALHAATGGIPILAGETYLICSEIPKLVPAVSTLGLGVWENUTAHADYVI 344

285 GTSLSITGTPTBEIRALHAATGGIPILAGETYLICSEIPKLVPAVSTLGLGVWENUTAHADYVI 344

345 QTTRNGVRCLSLSGFQLADDVPPFPFWIQLPFLIGTYAVFDRCDMKSSARVGLR 400

345 KVSAGGETICLSSLGFRGLDYPVPPGSPLWLIGDVFTGPyQJTGQFKA 396

KRHUD cathepsin D (EC 3.4.23.5) precursor [validated] - human  
 K: Alternative names: procathepsin D  
 C: Species: Homo sapiens (man)  
 C: Date: 28-Dec-1987 #sequence revision 28-Dec-1987 #text\_change 15-Sep-2000  
 C: Cross-references: GR:574689; PIDN:9786350; PIDN:AA014156.1; PID:942611856  
 R: Faust, P.L.; Kornfield, S.; Chirgwin, J.M.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 4910-4914, 1985  
 A: Title: Cloning and sequence analysis of cDNA for human cathepsin D.  
 A: Reference number: A25771; MUID:85270436; PMID:3927292  
 A: Accession: A25771  
 A: Molecule type: mRNA  
 A: Residues: 1-412 <FAU>  
 A: Cross-references: EMBL:M11233; NID:9181179; PIDN:AAB59529.1; PID:9181180  
 R: Westley, B.R.; May, F.E.B.; Smith, D.J.; Westley, B.R.  
 Nucleic Acids Res. 15, 3773-3785, 1987  
 A: Title: Oestrogen regulates cathepsin D mRNA levels in oestrogen responsive human breast  
 A: Reference number: S30749; MUID:87231068; PMID:3588310  
 A: Accession: S30749  
 A: Molecule type: mRNA  
 A: Residues: 1-412 <WES>  
 A: Cross-references: EMBL:X5344; NID:929677; PIDN:CBA28955.1; PID:929678  
 R: May, F.E.B.; Smith, D.J.; Westley, B.R.  
 Gene 134, 277-282, 1993  
 A: Title: The human cathepsin D-encoding gene is transcribed from an estrogen-regulated a  
 A: Reference number: PC2066; MUID:94085791; PMID:8262386  
 A: Accession: PC2066  
 A: Molecule type: DNA  
 A: Residues: 1-23 <MAY>  
 A: Cross-references: GB:L112980; NID:g291930; PIDN:AAA16314.1; PID:9455429  
 A: Experimental source: MCP-7 cell  
 R: Cavallais, V.; Augerau, P.; Rochefort, H.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 203-207, 1993  
 A: Title: Cathepsin D gene is controlled by a mixed promoter, and estrogens stimulate on  
 A: Reference number: 159236; MUID:93126342; PMID:8419924  
 A: Accession: 159236  
 A: Status: translation not shown; translated from GB/EMBL/DDBJ  
 A: Molecule type: DNA  
 A: Residues: 1-22 <CAV1>  
 R: Augerau, P.; Miralles, F.; Cavailles, V.; Gaudelat, C.; Parker, M.; Rochefort, H.  
 Mol. Endocrinol. 8, 693-703, 1994  
 A: Title: Characterization of the proximal estrogen-responsive element of human cathepsin  
 A: Reference number: 157716; MUID:95021301; PMID:7935485  
 A: Accession: 157716  
 A: Status: translation not shown; translated from GB/EMBL/DDBJ  
 A: Molecule type: DNA  
 A: Residues: 1-22 <CAV2>  
 A: Cross-references: GR:S52557; NID:9263124; PIDN:AA013868.1; PID:94261568  
 R: Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.  
 Submitted to the Brookhaven Protein Data Bank, April 1993  
 A: Contents: annotation: A51839; PDB:1LYA  
 Submitted to the Brookhaven Protein Data Bank, April 1993  
 A: Reference number: A51840; PDB:1LYB  
 A: Contents: annotation: X-ray crystallography, 2.5 angstroms, with inhibitor residues 65  
 R: Baldwin, E.T.; Bhat, T.N.; Gulnik, S.; Erickson, J.W.; Sowder II, R.C.; Cachau, R.E.; Col  
 Proc. Natl. Acad. Sci. U.S.A. 90, 6796-6800, 1993  
 A: Title: Crystal structures of native and inhibited forms of human cathepsin D: implicat  
 A: Contents: annotation: A88229; MUID:93332076; PMID:8393577  
 A: Title: Crystallography, 2.5 angstroms  
 C: Comment: Cathepsin D is a ubiquitous lysosomal protease.  
 C: Comment: In addition to the propeptide, residues 163-168 and 411-412 are proteolytical  
 C: Comment: The carbohydrate bound to 134-Aen contains a mannose-6-phosphate that is boun  
 C: Genetics:  
 A: Gene: GDB:CTSD  
 A: Cross-references: GR:D120512; OMIM:1168410  
 A: Map position: 1ip15.5-1ip15.5  
 C: Function:  
 A: Description: Limited specificity endopeptidase  
 A: Pathway: Intracellular protein degradation  
 C: Superfamily: pepsin

C:Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradat  
 F:1-20/D domain: signal sequence #status predicted <SIG>  
 C:Cross-references: PRO: #status predicted <PRO>  
 R:65-162,169-410/Domain: cathepsin D #status experimental  
 F:267,329-556/Region: phosphotransferase recognition  
 F:91-160,110-117,286-290,329-366/Disulfide bonds: #status experimental  
 F:134,263/Binding site: ASP #status experimental  
 F:134,263/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 Query Match Score 45.4%; Length 412;  
 Best Local Similarity 46.9%; Pred. No. 6.7e-77;  
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;  
 Qy 1 MSPPPHIOPQULLPLPLNVEPSGATLRIPLHRVOPGRRTNLRLRGWRE----PAELP 54  
 Db 1 MQPSLPLALLL--AAPASA-LVRIPHFKTSIRRMNTSVEGSVEDLIJKGVSKY 55  
 55 KLGAPSPGDKDPLFVPLNSYRQYFGBIGLGTTPQNFNTVAFTDTGSSNLWVPSRRCHFFSV 114  
 56 SQAVPAVTEGP1PEVKNYMDAQYSEIGIGTPQQCETVYDGTGSSNLWVPSIHKXLDDI 115  
 115 PWLHLHRFDPKASSSFANGTKPAIQYQTRGVDFGQDLSSEDKUTI-----GGTIGKA 163  
 116 ACWTHKXNSDKSSTYVNGKTSFDTIHYGSGLSGVLSQDTVSVCQASSASALGASYKVE 175  
 Qy 164 SVTGFALWEPSLVFAFAHDFGILGLGFPILSVEGRPPMDVLVBQSLDRPVSFLTQLCKEPLN 223  
 Db 176 RQVFGTAKPGITIAAKFCGILGMQNLVDNONIFSYLRS 235  
 224 DPEEPDGEGYLVGGSDPAHYIPLPTEVPPVTPAYWOTHMERYVKGPGLTCAKGCAAILD 283  
 236 DDDAQPGEMLGGTDKSKYRGSLSYLNVTRKAYWHDVEASGLTLCQEGCEAVD 295  
 Qy 284 TGTSLITGPTBEIRALHAAGISGPIPLAGEYILCSEPKLPAVSTLGGWMNLTHDYV 343  
 Db 296 TGTSLMVGPDYERLQKAIGAVPLQGETMPCERKVSTLPATIKLGIGKYLSPEDYT 355  
 Qy 344 IQRTRRNQVRLCLGQFQALDVPPGAPGPWILGDVFLLVYAFDRGDMKSSARVGLARA 401  
 Db 356 LKVSQAGKTCLSGFMGMDIPPSGLWLSDVFIGRYTYFDR---DNRRVGFPEA 409  
 RESULT 3  
 KRTD cathepsin D (EC 3.4.23.5) precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Accession: S11111; MUID:91057150; PMID:2243802  
 R:Birch, N.P.; Loh, Y.P.  
 A:Title: Cloning, sequence and expression of rat cathepsin D.  
 A:Reference number: S13111; MUID:91057150; PMID:913111  
 A:Accession: S13111  
 A:Molecule type: mRNA  
 A:Residues: 1-407 <BTR>  
 A:Cross-references: EMBL:X54467; NID:955881; PIDN:CAA38349.1; PID:g55882  
 R:Yonezawa, S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartlaub, J.A.; Tang, J.  
 J. Biol. Chem. 263, 16504-16511, 1988  
 A:Title: Structure at the proteolytic processing region of cathepsin D.  
 A:Reference number: A92681; MUID:89034127; PMID:3182800  
 A:Accession: C319118  
 A:Molecule type: Protein  
 A:Residues: 134-162, T, 164-170 <YON>  
 A:Residues: 1-14, 'A', 16-204, 'N', 206-261, 'N', 263-407 <FUU>  
 A:Accession: PQ0222  
 A:Molecule type: protein  
 A:Residues: 65-74;118-127;165-174 <FUU>

A;Experimental source: liver  
 C;Function: Cathepsin D in rat liver lysosome occurs as a mixture of both a single chain  
 C;Comment: limited specificity endopeptidase  
 A;Description: intracellular protein degradation  
 C;Superfamily: pepsin  
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation  
 F;21-64/Domain: proteptide #status predicted <PRO>  
 F;65-407/Product: cathepsin D, 43K single-chain form #status predicted <MAT>  
 F;65-164/Product: (or 65-165) cathepsin D 12K light chain #status predicted <MA2>  
 F;65-117/Product: cathepsin D 9K light chain #status predicted <MA4>  
 F;118-407/Product: cathepsin D 34K heavy chain #status predicted <MA5>  
 F;165-407/Product: (or 165-407) cathepsin D 30K heavy chain #status predicted <MA3>  
 F;91-160,110-117,281-324-361/Disulfide bonds: #status predicted  
 F;97,290/Active site: Asp #status predicted  
 F;134,258/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F;134,258/Binding site: carboxyhydrate (Asn) (covalent) #status predicted

Query Match 44.9%; Score 1005; DB 1; Length 407;  
 Best Local Similarity 48.3%; Pred. No. 4.5e-16;  
 Matches 196; Conservative 68; Mismatches 124; Indels 18; Gaps 4;

Qy 10 LLLPLUNVEPGATLIRPLHRVQPGRRTINLLRGWRE----PAELPKLGAPSPGD 63  
 Db 7 LLLLGLH---DASSSALLRPLRKETSIIRRMTTEVGSVEDLILKGPIKYSMQSSPRTK 64

Qy 64 KPIFVPLSNTRDVQXFGGEIGLGTGPONFTYAFDTGSNNLAWPSRRCHFESVPCWNLHFRD 123  
 Db 65 EPVSELLKINYLDAQYIYGIGTTPQQCTTVFDTGSNNLWPSIHKLIDACWHHKIN 124

Qy 124 PKASSSFQANGTKFAIQYGTGRVDGILSED-----KLTTGGIKGASVIFGEALMEPSLV 177

Db 125 SDKSSTIVVKNGNTSFHDHGSSLSGSLQDVTVSPEKSDIUGKVEKQIGEATKQPGVH 184

Qy 178 FAFAHFDGLLGFPPLISVEGVPPRPMDVLVBQGILDKPVPESFYLNARDPFDGGELVIGG 237  
 Db 185 FTAAKPDGLLNGYPPTSNKKVLPVDFNLNKQKLVEKNIFFYLNRDPTCPGPGEMLMGG 244

Qy 238 SDPAHVYPLTFVPPVTPVATPWQ1HMERKVVPGLTLCAKGAAILDTSNLTGPTEER 297

Db 245 TDSRYFHGSLSYNTRKAYMVOENMDOLEVSENLICKGGEAIVDTGSELLVGVDEVK 304

Qy 298 ALHAATIGGIPPLAGEYLILCSEIPKLPAVSTLGGYWENLTAHDYVICTFRNGYRLCLSG 357

Db 305 ELQKATGAVPLQGENMPCEKVSSELIITPKLGKGNYLRPEKTCILSG 364

Qy 358 FOALDYPPPAGPFWLIGDWFELGTYYAVFDRGSMKSSARVGLARAT 403  
 Db 365 FMGMDTIPPSPLWLIGDVFQGXYTTFDR---EYNRVCFAKAAT 406

RESULT 4  
 KMMSD  
 cathepsin D (EC 3.4.23.5) precursor - mouse  
 C;Species: Mus musculus (house mouse)  
 C;Accession: I48278; S14704; S12587  
 C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text\_change 18-Jun-1999  
 R;Heim, M.; Perschl, A.; Saating, P.; von Figura, K.; Peters, C.  
 DNA Cell Biol. 13, 419-427, 1994  
 A;Title: Mouse cathepsin D gene: molecular organization, characterization of the promoter  
 A;Reference number: 148278; PMID:94280622; PMID:8011168  
 A;Status: Preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-410 <RES>  
 A;Cross-references: EMBL:X68378; NID:950302; PIDN:CAA48453..1; PID:9817945  
 R;Dierich, J.F.; Stasikus, K.A.; Retzel, E.F.; Haase, A.T.  
 Nucleic Acids Res. 18, 7184, 1990  
 A;Accession: S14704; MUID:91088345; PMID:22633503  
 A;Molecule type: mRNA  
 A;Residues: 1-410 <DIE>

RESULT 5  
 A45117  
 aspartic proteinase (EC 3.4.23.-), lysosomal - yellow fever mosquito  
 C;Species: Aedes aegypti (yellow fever mosquito)  
 C;Date: 17-Feb-1994 #sequence\_revision 17-Feb-1994 #text\_change 22-Jun-1999  
 R;Cho, W.L.; Raikhel, A.S.  
 J. Biol. Chem. 267, 21823-21829, 1992  
 A;Accession: A45117  
 A;Title: Cloning of cDNA for mosquito lysosomal aspartic protease. Sequence analysis  
 A;Reference number: A45117; MUID:93016141; PMID:1400492  
 A;Status: Preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-387 <CHO>  
 A;Cross-references: GB:M95187; NID:g293229; PIDN:AAA29350..1; PID:9293230  
 A;Experimental source: fat body  
 A;Sequence extracted from NCBI backbone (NCBIN:116753, NCBI:116754)

C; Superfamily: pepsin  
 C; Keywords: aspartic proteinase; hydrolase; lysosome  
 F; 103-344 Product: cathepsin D light chain #status experimental <CDH>  
 F; 103-344 Product: cathepsin D heavy chain #status experimental  
 F; 33-272/Active site: Asp #status predicted  
 F; 46-53 Active site: Asp #status predicted  
 F; 46-53-220-224-263-300 Disulfide bonds: #status predicted  
 F; 70-197/Binding site: carbohydrate (Asn) (covalent) #status experimental  
 F; 287/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 43.1%; Score 964.5; DB 2; Length 387;  
 Best Local Similarity 48.5%; Pred. No. 1e-72;  
 Matches 192; Conservative 62; Mismatches 131; Indels 11; Gaps 5;

Qy 6 LIQPLLIJPLINVEPSGATLIRIPIRHPVQGRRTINILRGWREPAEPKLGAPSPODKP 65  
 Db 2 LIKSITIAVCLAVL--SQADEFRVQLEKTESARQHFRNVDTEIKQLRL-KTNAVS --GP 55

Qy 66 IFVPLSNTRDVOYFGEGLGTPQNFTVADTGSSNLWVPSRRCHFFSVPCKMLHREFDPK 125  
 Db 56 VPEPLSNVLDQAYGAATIGPQQSPKVFEDTGSSNLWVPSKECFNTIACLMENYRAK 115

Qy 126 ASSSFQANGTKFAIQLQYGRDVGILSLDKDTIGGKASVIFGEALMEPSLIVFAAHFDG 185  
 Db 116 KSSTPERKGTAHTIQIGSSLSGLSYLSTDVGGLGVSYTKQFQAETINEPGLYVFAAKFDG 175

Qy 186 IIGLGFPLLSVEGVPRPPMDVLYVBOQHJDKPVFSFYLNRDPEPDGGFLVLGCGSDPAHYIP 245  
 Db 176 IIGLGSYISLSDGVPVYNNMNQGLIDAPVSEFSYLNRDPSAEGGFIIGGSDSNKYG 235

Qy 246 PTEFVPVTPVPAIQHMERVKUGPGSLTICAKCQAAILDTGTSLITGPTEKEIRALHAIGG 305  
 Db 236 DFTYLSVRKAQWFKNDSVKVG-DTEFCNNGCEATAATDTGTSLIRAGPVSEVTAINKAIGG 294

Qy 306 IPILLAGEVILLOSEPKPAPASVFLGPQEWVNLTIAHDVYIQTTRNGVRLCLSGFOALDVP 365  
 Db 295 TPIMNGEYMVDSLIPKPKISFLVQGKSPDFLEGADYVLRVAQMGMKTICLQSGFMGIDIPP 354

Qy 366 PAGPFWILGDVFVGTYYVAFDRGDMKSSARVGLARA 401  
 Db 355 PGNGPLWILGDVFVGTYYVAFDRGDMKSSARVGLARA 386

RESULT 6  
 KPGD cathepsin D (EC 3.4.23.5) - pig  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 18-Apr-1984 #sequence revision 31-Dec-1991 #text\_change 18-Mar-1997  
 R;Takahashi, T.; Tang, J.  
 J. Biol. Chem. 258, 6435-6443, 1983  
 A;Title: Amino acid sequence of porcine spleen cathepsin D light chain.  
 A;Reference number: A92425; PMID:6406481  
 A;Accession: A92425  
 A;Molecule type: protein  
 A;Residues: 1-95; 'S' 97 <TA>  
 A;Experiment: 1 source: spleen  
 R;Shewale, J.G.; Tang, J.  
 Proc. Natl. Acad. Sci. U.S.A. 81, 3703-3707, 1984  
 A;Title: Amino acid sequence of porcine spleen cathepsin D.  
 A;Reference number: A93990; PMID:6587385  
 A;Accession: A93990  
 A;Molecule type: protein  
 A;Residues: 103-344 <SHE>  
 A;Experimental source: spleen  
 A;Note: 233 Lys and 246-Gln were also found  
 R;Yonezawa, S.; Takahashi, T.; Wang, X.; Wong, R.N.S.; Hartsuck, J.A.; Tang, J.  
 J. Biol. Chem. 263, 16504-16511, 1988  
 A;Title: Structures at the procolytic processing region of cathepsin D.  
 A;Accession: B31918  
 A;Molecule type: mRNA  
 A;Residues: 74-146 <YN>  
 A;Note: the sequence from Fig. 1 is inconsistent with that from Fig. S6 in having an add  
 C;Function:  
 A;Description: Limited specificity endopeptidase  
 A;Pathway: intracellular protein degradation  
 C;Superfamily: pepsin  
 C;Keywords: aspartic proteinase; glycoprotein; hydrolase; lysosome; protein degradation

Query Match 42.6%; Score 954.5; DB 1; Length 344;  
 Best Local Similarity 52.9%; Pred. No. 5.9e-72;  
 Matches 183; Conservative 48; Mismatches 102; Indels 13; Gaps 3;

Qy 65 PIFVPLSNTRDVOYFGEGLGTPQNFTVADTGSSNLWVPSRRCHFFSVPCKMLHREFDP 124  
 Db 2 PIPEVKNYMDAQYXGEIGLGPQCFCFVYEDTGSSNLWVPSIHKSKLDEACWIHKYNS 61

Qy 125 KASSSFQANGTKFAIQLQYGRDVGILSLDKDTIGGKASVIFGEALMEPSLIVFAAHFDG 175  
 Db 62 GKSSSTYVKGNTFPAHYGSSLSGVLSQDPTSVPCNSALSGVGGK1KVEROTFGEZTKOPG 121

Qy 176 LVFAFAHFDGILGLGPILSYEVPPMDVLYVEQGLDKEPVFSYLNRDPEPDGGELVL 235  
 Db 122 LTFLIAKFDGLGMAPRISTNNVVNPVFDNIMQQLVDDKLFSTFLNRDGAQPGEML 181

Qy 236 GGSDPAHYIPPLTFVTPVPAIQHMERVKUGPGSLTICAKCQAAILDTGTSLITGPTEKEIRALHAIGG 295  
 Db 182 GGDSKYKGSIDLVYINTRKAYWQTHMNOAVGSSLTLCRKGECAAVDTGTSLITGQPEE 241

Qy 296 IRLHHAIGGPPLLAEYIILCSEPKLPASVFLGPQEWVNLTIAHDVYIQTTRNGVRLCL 355  
 Db 242 VRELGTAIGAVPLQCEYMPCEKVPSPSLPDYTVTLGGKVKLSSSENLYTKVSOAQCTICL 301

Qy 356 SGFOQADVPPVPPAFWNLGDFVFLGTVVAFDRGDMKSSARVGLARA 401  
 Db 302 SGFMGMIDIPPFQGPMLGDFVIGRYYTVDPR-DIN--RVGLAEA 343

RESULT 7  
 T24204 hypothetical protein R12H7.2 - Caenorhabditis elegans  
 C;Species: Caenorhabditis elegans  
 C;Sequence: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 18-Feb-2000  
 C;Accession: T24204  
 R;Coles, L.  
 Submitted to the EMBL Data Library, August 1995  
 A;Reference number: Z19854  
 A;Accession: T24204  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-444 <NTL>  
 A;Cross-references: EMBL:Z50755; PIDN:CAA90633.1; GSPDB:GN00028; CESPP:R12H7.2  
 A;Experimental source: clone R12H7  
 C;Genetics:  
 A;Gene: CESPP:R12H7.2  
 A;Map Position: X  
 A;Introns: 29/2; 91/3; 133/1; 214/1; 395/2  
 C;Superfamily: pepbin

Query Match 40.5%; Score 905.5; DB 2; Length 444;  
 Best Local Similarity 49.7%; Pred. No. 1e-67;  
 Matches 166; Conservative 58; Mismatches 105; Indels 5; Gaps 2;

Qy 70 LSNYRDVQYFGEGLGTPQNFTVADTGSSNLWVPSRRCHFFSVPCKMLHREFDPKASSS 129  
 Db 86 LRNYMDAQYFSTISGTPAONFTVADTGSSNLWVPSKCKPFYDIACMHLHYDKSSS 145

Qy 130 FQANGTKFAIQLQYGRDVGILSLDKDTIGGKASVIFGEALMEPSLIVFAAHFDG 175  
 Db 146 YKEDGRKMAIQGTMGKFSKDSVVCVAGYCAEDOPFADATSEGTYVAAKPGFILGM 205

Qy 190 GFPILSYEVPPMDVLYVEQGLDKEPVFSYLNRDPEPDGGELVLGGSPDAHYIPLTF 249  
 Db 206 AYPEIAVGLGVQEVNTLFEQRKVPSPNLFWLNRPDSRIGGETFGGIDSRRYVEPITY 265

Qy	250	VPTVTPAYQIHMERVKVGPGLTCAKGCAAILDTGTSILITGPEETRALHAAIGGPL 309	F;18/Modified site: blocked amino end (Gln) (in mature form) (probably pyrrolidine ca F;16,283/Active site: Asp #status predicted
Db	266	VPTRPKGYTQFKDKV-YGSQVLGCNSNGQAIADTGTSGIAAGKAQIEAQNFQGAFFI 324	Query Match 38.8%; Score 869; DB 2; Length 396;
Qy	310	AGETYTILCSEIPKLPAVSPFLLGGWENLTAHDYVIQTRNGVRCLSLCFQALDVPAPP 369	Best Local Similarity 45.1%; Pred. No. 9.e-65;
Db	325	KGEYNISCDKVTPLPVSFVIGGDFBSLXGEDTVLKVSOGGTTICLSGFMGIDLPERYE 384	Matches 179; Conservative 70; Missmatches 136;
Qy	370	EWLIGDVEFLGTYYAVEDRDMKSSARVGLARART 403	Indels 12; Gaps 5;
Db	385	LWLIGDVEFGRYYSVF---FDONRVRGAQAKT 414	Qy 10 LLLLPLINVERPGATLIRPLHVRQPGRRTL---NLLRGWR-EPAELPKLGAPSPPDK 64
	RESULT 8	5 LLLLVLLEAQGSLLHRVPLRRHPSLKKLRARSQLESEFNKSHNLDMIQFTESCSNDQ 64	
	A34401	cathepsin E (EC 3.4.23.34) precursor - human	65 PIFVPLSNYRDVOYFGEIGLGPQNFTVAFDTGSNNDWPSRCHFSVPCTLHHRFPD 124
C;Species:	Homo sapiens (man)	65 SAKEPLINYLDMEFGTISIGSPQQNFNTVAFDTGSNINWPSVYC-TSPACKTHSRFPQ 122	
C;Accession:	A42038; A34401; B34643; B3463	Db 125 KASSSFQANGTKPAIQXTGVRDVGILSNDKLTIGGIKGASVLFGEALWEPSLVYFAFAHFD 184	
R;Izuma, T.; Liu, W.; Vander Laan, D.J.; Bowcock, A.M.; Taggart, R.T.	Db 123 SQSTTYSQGQPSFIIQXGTGSGIAGDQVSBGILTIVQQGESEVTEPGQDFVDAEFD 182		
J. Biol. Chem. 267, 1639-1614, 1992	Qy 185 GIIGLGFPLSVEGVPPMDVLVEQGLLDPKPVFSFLYRDPPEPDGGLVLLGGSDPAHYI 244		
A;Title: Human gastric Cathepsin E gene. Multiple transcripts result from alternative po	Db 183 GILGLGYSLSAVGCTTPYFDNNMAQNLVDLPMFSVYMSNPSEGAGSPLIFCGYDHSHFS 242		
A;Accession: A42038; MUID:1370478	Db 245 PPIITFPVTPVPAWQIHMERVKVGPLGLTCAKGCAAILDTGTSLITGPTEEIRALHAIG 304		
A;Molecule type: DNA	Db 243 GSINWWVPTKQATWQIALDNIQVGTVMFCSEGCQAIWDTGTSLITGPDSKIKQLQNAIG 302		
A;Residues: I-396 <AZU>	Db 305 GIPLLAGETYLILSEIPKLPAPAVFLGGYWENLTAHDYVTCUTRNGYRLCLSCFQALDYP 364		
A;Cross-references: GB:M82847; GB:M82847; PID:g181203; PID:AAA52300.1; PID:g181205	Qy 303 AAP-VDGEYAVECANLYMPDVTTINGVPTYUSPATYLLDEFDGMOCSSGFQGLDIH 361		
R;Izuma, T.; Palis, G.; Mohandas, T.K.; Courteur, J.M.; Taggart, R.T.	Db 303 AAP-VDGEYAVECANLYMPDVTTINGVPTYUSPATYLLDEFDGMOCSSGFQGLDIH 361		
J. Biol. Chem. 264, 16748-16753, 1989	Qy 365 PPAPFWLIGDVFGLTYAVFDRGDMKSSARVGLARA 401		
A;Title: Human gastric cathepsin E. Predicted sequence localization to chromosome 1, and	Db 362 PPASPLWILGDVFTRQFTSVDERG---NNRVGLAPA 394		
A;Reference number: A34401; MUID:89380302; PMID:267441			
A;Accession: A34401			
A;Molecule type: mRNA			
A;Residues: I-396 <AZU>			
A;Cross-references: GB:J05036; PID:g181193; PID:AAA52130.1; PID:g181194			
R;Takeda-Ezaki, M.; Yamamoto, K.	RESULT 9		
Arch. Biochem. Biophys. 304, 352-356, 1993	S66465 cathepsin E (EC 3.4.23.34) precursor (clone pTM05) - rat		
A;Title: Isolation and biochemical characterization of procathepsin E from human erythrocytes	C;Species: Rattus norvegicus (Norway rat)		
A;Reference number: S35663; MUID:93349047; PMID:8346312	C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000		
A;Status: Preliminary	C;Accession: S66465; S74309		
A;Molecule type: protein	R;Okamoto, K.; Yu, H.; Misumi, Y.; Ikehara, Y.; Yamamoto, K.		
A;Residues: 20-384-76 <TAK>	Arch. Biochem. Biophys. 322, 103-111, 1995		
R;Bill, J.; Montgomery, D.S.; Kay, J.	A;Title: Isolation and sequencing of two cDNA clones encoding rat spleen cathepsin E		
FEBS Lett. 326, 101-104, 1993	A;Reference number: S66465; MUID:96004785; PMID:7574663		
A;Title: Human cathepsin E produced in E. coli.	A;Accession: S66455		
A;Reference number: S34467; MUID:93314762; PMID:8325357	A;Molecule type: mRNA		
A;Accession: S34467	A;Residues: 1-398 <OKA>		
A;Status: Preliminary	A;Cross-references: EMBL:D45187; NID:91113085; PIDN:BAA08128.1; PID:91113086		
A;Molecule type: protein	A;Accession: S74309		
A;Residues: 57-60, 62-81 <HIL>	A;Molecule type: protein		
R;Arribaud, S.B.P.; Matubzaki, O.; Kageyama, T.; Takahashi, K.	A;Residues: 20-47-59-91 <OKN>		
Biochem. Biophys. Res. Commun. 168, 878-885, 1990	C;SuperFamily: peptain		
A;Title: Structural evidence for two isozymic forms and the carbohydrate attachment site	A;Signal sequence: #status predicted <SIG>		
A;Reference number: A34463; MUID:90241267; PMID:2334440	F;1-19/Domain: F;20-58/Domain: peptide #status experimental <PRO>		
A;Accession: A34463	F;59-398/Product: cathepsin E #status experimental <MAT>		
A;Status: Preliminary	Query Match 39.7%; Score 867; DB 2; Length 398;		
A;Molecule type: protein	Best Local Similarity 45.3%; Pred. No. 1.4e-64;		
A;Residues: 54-58, XXX, '62-64, 'M', 66-89, 'X', 91-95 <AT2>	Matches 180; Conservative 68; Missmatches 137; Indels 12; Gaps 5;		
A;Accession: B34643	Qy 10 LLLLPLINVERPGATLIRPLHVRQPGRRTL---NLLRGWR-EPAELPKLGAPSPPDK 64		
A;Status: Preliminary	Db 7 LLLLVLLEAQGSLLHRVPLRRHPSLKKLRQGOLSDFWRSNLDMIEFSES CNDK 66		
A;Molecule type: protein	Qy 65 PIFVPLSNYRDVOYFGEIGLGPQNFTVAFDTGSNNDWPSRCHFSVPCTLHHRFPD 124		
A;Residues: 54-59, 'X', 61-68 <AT2>	Db 67 GINBPLINYDMEYYGTGSTGSPSSNFTVAFDTGSNINWPSVTC-TSPACKHAPVFP 124		
C;Genetics:	Qy 125 KASSSFQANGTKPAIQGTRDVGILSEDKLIGKGAISVGRALWPSLVYFAFAHFD 184		
A;Gene: GDB:CTSE			
A;Map position: 1q31-1q31			
C;Superfamily: peptain			
C;Key words: aspartic proteinase; blocked amino end; hydrolase; zymogen			
F;1-17/Domain: signal sequence #status predicted <SIG>			
F;18-53/Domain: activation Peptide #status predicted <PRO>			
F;54-396/Product: cathepsin E #status predicted <MAT>			

RESULT 11  
S11697  
Soybean trypsinase (EC 3.4.23.-) precursor - barley

C;Species: Hordeum vulgare (barley)  
C;Accession: SI11697  
C;Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 22-Jun-1999  
R:Runenberg-Roos, P.; Toermaekangas, K.; Oestman, A.  
Bur. J. Biochem. 202, 1021-1027, 1991  
A;Title: Primary structure of a barley-grain aspartic proteinase. A plant aspartic proteinase from barley grain  
A;Reference number: S11697; MJD:92111473; PMID:1722454  
A;Accession: S11697  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-508 <RUN>  
A;Cross-references: EMBL:X56136; PIDN:CAA39602.1; PID:gi18904  
A;Comment: The pair of saposin repeat homology domains tagged SAP1 and SAP2 reported by Runenberg-Roos et al. (1991) is identical to the sequence of the saposin repeat domain of the primary structure of the soybean trypsinase precursor protein.  
C;Superfamily: oryzain: Saposin repeat homology  
C;Keywords: aspartic proteinase; hydrolase  
F;315-360/Domain: saposin repeat homology #status atypical <SAP1>  
F;319-419/Domain: saposin repeat homology #status atypical <SAP2>  
F;102,289/Active site: ASP #status predicted

Query Match Score 830; DB 2; Length 508;  
Best Local Similarity 36.7%; Pred. No. 2 4e-65;  
Matches 186; Conservative 54; Mismatches 247; Gaps 7;

Qy 6 LLQPLILILLPLLNVPMSGATLIRIPHRVQPERRTIILNLGRWREPAAPLKQGAPSPP--- 61  
Db 10 ILAAVLLIQTLPLPAASEAGLYTRIAEKKRDPDNRSSVATGIGSGGEQPLUSGANPURSE 68

Qy 62 --GDKPPIFPVPLSNYRDQYFGIGLGPQPNQNTVAPDTGSSNLWVPSRRCHFEFSPCPWLH 119  
Db 69 BEGD--IVAKLKNMNYQQFGEGVGTPPOKETVIFDTGSSNLWVPSAKC-YFISIACYLH 124

Qy 120 HRFDPKASSFQANGTKFAIQYGTGRYDGLSESKDQITGGIKGASVTFGEALWEPFLYFA 179  
Db 125 SRYKAGASSTYKONGKPAAIQGTGSLAGYFSESDVTFATKEPGITL 184

Qy 180 FAHDGIGLGLGFPLSVEGVPRPMDVLEQGLIDPKVFSYLVNRLDPEPDGSLVLVLGSD 239  
Db 185 VAKFDGIGLGLGFKRSVKAQPVWYKMEQGLVSDPFSWLRHVDGEGBIIFFGMD 244

Qy 240 PAHYIPLTPEVPTVPAWQHMERVKVPGPLT-LCAKGCAAIIDTGTSLTGPTEEIRA 298  
Db 245 PKHYVGEEETVPTVQKGWQFDNGDVLYGGKSTGFCAAGCAAAADSGTSLLAGPTAITE 304

Qy 299 LHAJIGG----- 305  
Db 305 INEKIGAAGVVSQECKTIVSQYQGQIQLDILLABTOPKKKICSOVGLCTFDGTRGVSAIGRS 364

Qy 306 ----- 314  
Db 365 VVDDEPVNSGLRADPMCSACENAVVMVNQNLAQNKTDQILDLYVNQLCNRLPSPMGESA 424

Qy 315 ILCSEIPKLPAPAVSFLLGGTYWENLTAHDYVIQTGTVLGSARVGLARA 401  
Db 425 VDCSSLGSMPDIEFTGGKKFALKREPEYILKVGEGAAAOCISGFTAMDIPPRGPWLIG 484

RESULT 12  
REMS  
C;Species: Mus musculus (house mouse)  
C;Date: 15-Oct-1982 #sequence\_revision 17-Dec-1982 #text\_change 18-Jun-1999  
R:McDonald, K.S.; Chang, J.J.; Inagami, T.  
Proc. Natl. Acad. Sci. U.S.A. 79, 4858-4862, 1982  
A;Title: Amino acid sequence of mouse submaxillary gland renin.  
A;Reference number: A93923; MUID:63014991; PMID:6812055  
A;Accession: A93923  
A;Molecule type: protein  
A;Residues: 64-351;54-01 <MIS>

R;Panthier, J.-J.; Foote, S.; Chambraud, B.; Strosberg, A.D.; Corvol, P.; Rougeon, F. Nature 298, 90-92, 1982  
A;Title: Complete amino acid sequence and maturation of the mouse submaxillary gland renin  
A;Reference number: A93285; MUID:8283373  
A;Accession: A93285  
A;Molecule type: mRNA  
A;Residues: 1-98; 'M', 100-194; 'LRSR', 199-394; 'V', 396-401 <PA1>  
A;Cross-references: GB:J00621; GB:V00845; NID:9200701; PID:NAA40050.1; PMID:9200702  
A;Note: the authors translated codon ATG for residue 99 as Ile  
A;Accession: B9285  
A;Molecule type: protein  
A;Residues: 64-84; 354-374 <PA2>  
R;Poe, M.; Liesch, J.M.; Biol. Chem. 258, 9856-9860, 1983  
A;Content: annotation; fatty acid binding  
R;Panthier, J.J.; Dreyfus, M.; Roux, D.T.L.; Rougeon, F.  
Proc. Natl. Acad. Sci. U.S.A. 81, 5489-5493, 1984  
A;Title: Mouse kidney and submaxillary gland renin genes differ in their 5' putative regulatory regions  
A;Reference number: A22056; MUID:8229816; PMID:609205  
A;Accession: B22056  
A;Molecule type: DNA  
A;Residues: 1-29 <PA3>  
C;Comment: The enzyme contains a noncovalently attached fatty acid.  
C;Comment: Submandibular renin has catalytic and antigenic activities similar to renal renin.  
C;Comment: This renin is synthesized in the submandibular gland of males only.  
C;Genetics:  
A;Gene: REN2  
C;Superfamily: Pepsin  
C;Keywords: aspartic proteinase; hydrolase; salivary gland; submandibular gland  
E;1-21/Domain: signal sequence #status predicted <SIG>  
E;22-63/Domain: activation peptide #status predicted <ACP>  
F;354-401/Product: renin, submandibular, heavy chain #status experimental <RSH>  
F;354-401/Active site: Asp #status experimental <RSL>  
F;101,286/Active site: Asp #status experimental <ASP>  
F;114-121,277-281,320-357/Disulfide bonds: #status predicted  
Query Match 36.1%; Score 808.5; DB 1; Length 401;  
Best Local Similarity 41.7%; Pred. No. 1.1e-59;  
Matches 172; Conservative 62; Mismatches 147; Indels 31; Gaps 7;  
Qy 5 PILLQPILLPLLNVPSPGATLIRIPLHRVOPGRRTLNLRGWREPAELPKLGAP --- 59  
Db 7 PLWALLWLSPLCTSFELPTGTFFERIPKRM-PSVREILLEERG---VDMTRLSAENDVFT 61  
Qy 60 -----SPCDKPFLFPVPLSNSYRDVOYFGRIGLGTSPQNPNTVAEDTGSNLWVPSRRCH 110  
Db 62 KRSSLTDLISP-----VVLINLYNLSQYVFLGEGLGTPQTFKIVFDTGSNLWVPSTKCS 115  
Qy 111 FFSVPCWLHFRDPKASSQFQANGTKPAIQYGTGRDVGILSEDKLTIIGKKGASVIFGEA 170  
Db 116 RLYLACGCKHSYESSSSSYEMNGDDFTTHSGRTKGFLSQDSVTYVGFL-VTQTFGEV 174  
Qy 171 LWEPSLYFAFHDFGLLGPPILSYGVPPMDVILVEQGLLKEPVFSFTLNRDBEPDG 230  
Db 175 TELPLIPMLAQFDGVLGMPGAQVGGTVEFDHLSQVLTKEVPSVTVNRPFLH-G 233  
Qy 231 GELVLGSDPARYIPLTFVPTVTPAYWQTHMERYVKVPGFLCAKGCAAILDTGTLIT 290  
Db 234 GEVVLGSDPPHYQGDHYVSLSKDWTMKGVSQGSSFLLCBAGCIVVVDTSFFIS 293  
Qy 291 GPTEEIRALHAAGGIPPLAGBYIILCSEIPKLPAYSFLIGGGWFMNLTAHDYIOTTRG 350  
Db 294 APTSSRLIMQALGAKERKHEYYWVSCSQVPTLDISENULGRAVTLSTSDYVQPNRR 353  
Qy 351 VRLCLSGFQALDVPPAGPFWILGDVFGLTYVAVFDRGMKMSARVGLAZAR 402  
Db 354 DKLCTVAYLHANDIPIPPTGPVWVLAGTIRKEYTEFDR---HNRRIGFALAR 401

RESULT 14  
S66516  
oryzasin (EC 3.4.23.-) precursor - rice  
N;Alternate names: aspartic proteinase 1  
C;Species: Oriza sativa (rice)  
C;Date: 28-Oct-1996 #sequence\_revision 13-Mar-1997 #text\_change 20-Jun-2000  
C;Accession: S66516; S65517  
R;Asakura, T.; Watabane, H.; Abe, K.; Arai, S.  
Bur. J. Biochem. 232, 77-83, 1995  
A;Title: Rice aspartic proteinase, oryzasin, expressed during seed ripening and germination  
A;Reference number: S66516; MUID:7556174  
A;Accession: S66516  
A;Molecule type: DNA  
A;Residue: 1-509 <ASA>  
A;Accession: S66517  
A;Cross-references: EMBL:D32165; NID:9511665; PID:BA006876.1; PID:91030715  
A;Molecule type: mRNA  
A;Residue: 1-509 <ASZ>  
A;Cross-references: EMBL:D32144; NID:91255684; PID:BA006875.1; PID:91711289  
C;Comment: The pair of saponin repeat homology domains tagged SAP1 and SAP2 represent C;Genetics:  
A;Intron: 119/3; 140/1; 171/3; 209/2; 265/3; 279/1; 300/3; 338/3; 360/2; 412/3; 452/  
C;Superfamily: oryzasin; saponin repeat homology  
A43356

C;Keywords: aspartic proteinase; hydrolase		Matches: 160; Conservative 44; Mismatches 126; Indels 7; Gaps 2;
F;1-20/Domain: signal sequence #status predicted <SIG>		
F;21-48/Domain: propeptide #status predicted <PRO>		
F;49-509/Domain: aspartic proteinase 1 #status Predicted <MAT>		
F;316-361/Domain: aspartic proteinase 1 #status Predicted <MAT>		
F;370-400/Domain: repeat homology #status atypical <ASP1>		
F;410-420/Domain: repeat homology #status atypical <ASP2>		
Query Match 35.9%; Score 804; DB 2; Length 509;		
Best Local Similarity 36.4%; Pred. No. 3.6e-59;		
Matches 185; Conservative 51; Mismatches 146; Indels 126; Gaps 8;		
Qy 6 LIQPLILLPLINVEPGSAT--LIRILHHR--VQPGRRTNLILRGREPARLPKLGAPS- 60		
Db 15 LIQALL-----PASAEFGIVRALKKRPIDENNSRAARLSGEGARRGLRANSI 65		
Qy 61 --PGDKP1FLPVLSNYRDVQYFGRIGLPVPPQNFTVADTGSSNLWVPSRCHEFFSVCWL 118		
Db 66 GGGGGEGIVALKKYNMNAQYFGRIGVTPPKQKFETVTDGSNLWVPSAKC-YFSTACFF 124		
Qy 119 HHRFDPKASSFOANGTKFAIJOYGTGRVGDGILSEDKLUTIGGIKGASYVIFGEALWPSLVF 178		
Db 125 HSYKSGGSSSTYRKNGKREAAIQGTTGSAFGFSEDSVWVGDIVVVKOOFBIATKEPDLTF 184		
Qy 179 AFAHFDGIGLGIGPILSVEGVRRPMDDVLEQVSHLDKIVFESYVILNDRDEEPDGELVIGGS 238		
Db 185 MYAKFDGIGLGIGPQEISVGDAVSVWVQVMEQVHSEVSEPVSPFSEVNRHEDBEGEIVFGM 244		
Qy 239 DPARYIPLTFLPVTVPAWYQIHMERYTVKPGPLT-LCKNGCIALDPTGTSLITGPTEBIR 297		
Db 245 DPHYKGHHTYVVSQKGYWQFEMGDTVLJGKKTGFCSGSCSAIASTDCTSLLAGPAAIT 304		
Qy 298 ALHAAIGG----- 305		
Db 305 EINEKIGATGVVSOECKTVSQYQQIIDLLETOPKKICSQVGLCTFDKGKVSAQIK 364		
Qy 306 -----TPIILAGEY 313		
Db 365 SVYDEAEGSNGLOSSPMGNACMAVWMWNQLAQNKTQDLTINYINLCDKLPSPMNES 424		
Qy 314 IILCEIIPKLPAYSFLLGWVFNLTADHYVQITRNGTRLCKSGQFQALDVPPAGPTWIL 373		
Db 425 SVDGCSLASMPEISETIGAKKFALKPEEYLKVGEAAAQCISGFTANDIPPRGQLWIL 484		
Qy 374 GDVFLGTYTAYFDRGDMKSSARVGLARA 401		
Db 485 GDVFMGAHTVFDYGMK---RVGFAKS 508		
Search completed: June 2, 2004, 20:22:21		
Job time: 29.59 secs		

## RESULT 15

JCS077 aspartic proteinase (EC 3.4.23.-) - dog hookworm (*Ancylostoma caninum*) (fragment)

N;Alternate names: Acasp; cathepsin D homolog

C;Species: *Ancylostoma caninum*

C;Date: 31-Jan-1997 #sequence\_revision 31-Jan-1997 #text\_change 22-Jun-1999

C;Accession: JC5077

R;Harrop, S.A.; Prociiv, P.; Brindley, P.J.

Biochim. Biophys. Res. Commun. 227, 294-302, 1996

A;Title: Acasp, a gene encoding a cathepsin D-like aspartic protease from the hookworm *A*

A;Reference number: JC5077; MUID:9701129; PMID:8858139

A;Accession: JC5077

A;Molecule type: mRNA

A;Residues: 1-442 &lt;HAR&gt;

C;Cross-references: GB:U34888; NID:91507724; PID:AAB06575.1; PMID:91507725

C;Comment: This enzyme is allergenic in human and contributes to the segmental inflamma

C;Genetics:

A;Gene: Acasp

C;Superfamily: pepsin

C;Keywords: aspartic proteinase; hydrolase

F;106,296/Active site: Asp #status predicted

Query Match 35.9%; Score 803.5; DB 2; Length 442;

Best Local Similarity 47.5%; Pred. No. 3.3e-59;

16	1.037	4.6 .3	410	11	US-09-B33-245-710
	17	1.015	45.4	412	9 US-09-B35-450-25
	18	1.015	45.4	412	9 US-09-B53-955-12
	19	1.015	45.4	412	12 US-10-B75-107-39
	20	1.015	45.4	412	13 US-10-B114-164-12
	21	1.015	45.4	412	16 US-10-B601-091-25
	22	1.015	45.4	412	16 US-10-B08-765A-06
	23	1.002	44.8	440	12 US-10-B112-944-433
	24	905.5	40.5	444	15 US-10-B369-65962
	25	887	39.6	446	14 US-10-B20-083-2
	26	869	38.8	396	9 US-09-B15-450-22
	27	869	38.8	396	9 US-09-B53-956-13
	28	869	38.8	396	12 US-10-B621-283-9
	29	869	38.8	396	13 US-10-B134-164-13
	30	869	38.8	396	15 US-10-B295-027-179
	31	869	38.8	396	16 US-10-B188-832-54
	32	869	38.8	396	16 US-10-B601-091-22
	33	868	38.8	368	11 US-09-B33-245-707
	34	868	38.8	404	14 US-10-B698-6317
	35	828.5	37.0	514	14 US-10-B339-351-1
	36	825.5	36.9	514	14 US-10-B339-351-3
	37	815	36.4	507	12 US-10-B424-599-245585
	38	798.5	35.7	523	12 US-10-B25-114-57691
	39	793	35.4	376	15 US-10-B051-874-164
	40	790	35.3	374	15 US-10-B74-978A-134
	41	788	35.2	513	12 US-10-B425-114-46548
	42	788	35.2	513	12 US-10-B425-114-66071
	43	787	35.2	480	12 US-10-B425-114-65101
	44	787	35.2	513	12 US-10-B425-114-56631
	45	786	35.1	513	12 US-10-B425-114-57054

Prepared. No. is the number of results predicted by chance to have a score greater than or equal to the score of the test being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB ID	Description	
					Sequence 1	Sequence 2
1	223.8	100.0	420	12	US-09-968-415-4	Sequence
2	223.8	100.0	420	14	US-10-180-719-4	Sequence
3	223.2	99.7	420	14	US-10-288-222A-3.0	Sequence
4	223.2	99.7	433	9	US-03-964-999-11	Sequence
5	2069.-5	92.5	395	13	US-10-094-080-3	Sequence
6	1702.5	76.1	390	9	US-09-969-384-15	Sequence
7	1560.5	69.7	419	9	US-09-789-919-44	Sequence
8	13.28	59.3	262	11	US-09-15-582-66	Sequence
9	13.28	59.3	262	11	US-09-833-245-14-69	Sequence
10	12.28	59.3	262	14	US-10-277-802-66	Sequence
11	11.79	52.7	285	9	US-09-925-302-670	Sequence
12	11.79	52.7	285	12	US-09-925-302-670	Sequence
13	10.50	46.9	212	9	US-09-915-582-87	Sequence
14	10.50	46.9	212	11	US-09-833-245-14-71	Sequence
15	10.50	46.9	212	14	US-10-277-802-67	Sequence

RESULT 1  
US-09-368-415-4  
; Sequence 4, Application US/09966415  
; Publication No. US2002008334A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; Hillman, Jennifer L.  
; Yue, Henry  
; Guegler, Karl J.  
; Corley, Neil C.  
; Tang, Tom Y.  
; Shah, Purvi  
TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
NUMBER OF SEQUENCES: 24  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSEQ for Windows Version 2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/968,415  
FILING DATE: 26-Sep-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/659,151  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Mohan-Peterson, Sheela  
REGISTRATION NUMBER: 41-201  
REFERENCE/DOCKET NUMBER: PF-0458 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 420 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LUNGAST01

CLONE: 877617

SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

US-09-968-415-4

Query Match Score 2238; DB 12; Length 420;

Best Local Similarity 100.0%; Pred. No. 1 9e-209; Indels 0; Gaps 0;

Matches 420; Conservative 0; Mismatches 0; Single

DB 61 PGDKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

DB 61 PGKPKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

Qy 121 RFDPKASSFFQANGTKPFAIQYGTGRVDGILSBDKLTTGIGKASVIRGEALWEPSPLYFAF 180

Db 121 RFDPKASSFFQANGTKPFAIQYGTGRVDGILSBDKLTTGIGKASVIRGEALWEPSPLYFAF 180

Qy 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Db 181 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Qy 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Db 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Qy 241 AHYPPLTFVPPTVPAYQHMERVKVSPGLTCAKGAAILDGTSLITGTEETRALH 300

Db 241 AHYPPLTFVPPTVPAYQHMERVKVSPGLTCAKGAAILDGTSLITGTEETRALH 300

Qy 301 AATGGIPPLIAGETLICSSIPKPAVSTLGGFWNLTAHDVIVOTPGNGRLCISGQA 360

Db 301 AATGGIPPLIAGETLICSSIPKPAVSTLGGFWNLTAHDVIVOTPGNGRLCISGQA 360

Qy 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

Db 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

Qy 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

Db 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

RESULT 2

US-10-180-719-4

Sequence 4, Application US/10180719

Publication No. US20030166246A1

GENERAL INFORMATION:

APPLICANT: Bandman, Olega

Hillman, Jennifer L.

Yue, Henry

Giegler, Karl J.

Corley, Neil C.

Tang, Tom Y.

Shah, Purvi

TITLE OF INVENTION: HUMAN PROTEASE MOLECULES

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Dr.

CITY: Palo Alto

STATE: CA

COUNTRY: USA

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/180,719  
FILING DATE: 25-Jun-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/008,271  
FILING DATE: 16-Jan-1998

ATTORNEY/AGENT INFORMATION:

NAME: Monan-Peterson, Sheila  
REGISTRATION NUMBER: 41,301  
REFERENCE/DOCKET NUMBER: PF-0458 US

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-845-0555  
TELEFAX: 650-845-4166

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 420 amino acids

TYPE: amino acid

STRANDEDNESS: Single

TOPOLOGY: linear

IMMEDIATE SOURCE:

LIBRARY: LONGAST01

CLONE: 877617

SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

US-10-180-719-4

Query Match Score 2238; DB 14; Length 420;

Best Local Similarity 100.0%; Pred. No. 1 9e-209; Indels 0; Gaps 0;

Matches 420; Conservative 0; Mismatches 0; Single

DB 61 MSPPPLIQPLLLPLINVEPSGATLIRIPLHRVQPGRTINLLRGWREPAELPKLGAPS 60

Qy 1 MSPPPLIQPLLLPLINVEPSGATLIRIPLHRVQPGRTINLLRGWREPAELPKLGAPS 60

Db 1 MSPPPLIQPLLLPLINVEPSGATLIRIPLHRVQPGRTINLLRGWREPAELPKLGAPS 60

Qy 61 PGDKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

Db 61 PGKPKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

Qy 121 RFDPKASSFFQANGTKPFAIQYGTGRVDGILSBDKLTTGIGKASVIRGEALWEPSPLYFAF 180

Db 121 RFDPKASSFFQANGTKPFAIQYGTGRVDGILSBDKLTTGIGKASVIRGEALWEPSPLYFAF 180

Qy 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Db 181 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Qy 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Db 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Qy 61 PGDKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

Db 61 PGKPKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

Qy 61 PGDKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

Db 61 PGKPKPIFPLSNYRDQYFGEIGLGPQNFTYAFDGSNNLWPSRCHFSVPCWLHH 120

Qy 121 RFDPKASSFFQANGTKPFAIQYGTGRVDGILSBDKLTTGIGKASVIRGEALWEPSPLYFAF 180

Db 121 RFDPKASSFFQANGTKPFAIQYGTGRVDGILSBDKLTTGIGKASVIRGEALWEPSPLYFAF 180

Qy 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Db 181 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Qy 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Db 121 AHFDGILGLGFPLISVEGVPRPMMDVLYEQGLLDPGGLVLGGSDP 240

Qy 241 AHYPPLTFVPPTVPAYQHMERVKVSPGLTCAKGAAILDGTSLITGTEETRALH 300

Db 241 AHYPPLTFVPPTVPAYQHMERVKVSPGLTCAKGAAILDGTSLITGTEETRALH 300

Qy 301 AATGGIPPLIAGETLICSSIPKPAVSTLGGFWNLTAHDVIVOTPGNGRLCISGQA 360

Db 301 AATGGIPPLIAGETLICSSIPKPAVSTLGGFWNLTAHDVIVOTPGNGRLCISGQA 360

Qy 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

Db 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

Qy 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

Db 361 LDVPPPAGEFWLGDVFGLCTYAVAFDRGMKSARVGALARTRGADLGWGETAQAOFG 420

RESULT 3

US-10-288-222A-30

Sequence 30, Application US/10288222A

Publication No. US2003019742A1

GENERAL INFORMATION:

APPLICANT: Logan, Thomas Joseph

APPLICANT: Galvin, Katherine

APPLICANT: Chun, Miyoung

TITLE OF INVENTION: Methods and Compositions to treat Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 241

TITLE OF INVENTION: Cardiovascular Disease Using 10183, 10550, 12880, 17921, 32248, 60489 OR 93804

FILE REFERENCE: MP2001-2862R(M)

CURRENT APPLICATION NUMBER: US/10/288, 222A

CURRENT FILING DATE: 2002-11-05

NUMBER OF SEQ ID NOS: 30

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 30  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-288-22A-30

Query Match 99.7%; Score 2232; DB 14; Length 420;  
Best Local Similarity 99.8%; Pred. No. 7.3e-209; Indels 0; Gaps 0;  
Matches 419; Conservative 0; Mismatches 1;

QY 1 MSPPPLQLLPLNVEPSGATLIRIPLHRVQGRTRNLGRWRAEPLPKLGAPS 60  
Db 1 MSPPPLQLLPLNVEPSGATLIRIPLHRVQGRTRNLGRWRAEPLPKLGAPS 60

QY 61 PGDKP1FVPLSNYRDQYFGEIGLGTQNPNTVAFDTGSNLWPSRQHFFSVPWMUH 120  
Db 61 PGDKP1FVPLSNYRDQYFGEIGLGTQNPNTVAFDTGSNLWPSRQHFFSVPWMUH 120

QY 121 RFDPKASSQANGTKFAIYQTRGRDGVILSEDKLTTGIGKASVIFGHALWEPSSLVFAF 180  
Db 121 RFDPKASSQANGTKFAIYQTRGRDGVILSEDKLTTGIGKASVIFGHALWEPSSLVFAF 180

QY 181 AHFDGLGQFPILSVEGVRPMDDVLYEQGLDQPEEPGGELVIGGSDP 240  
Db 181 AHFDGLGQFPILSVEGVRPMDDVLYEQGLDQPEEPGGELVIGGSDP 240

QY 241 AHYIPPLTFTPVTPVTPAYWQIHMERVKVGQPLTLCKGCAAILDTGTSLLTGPIEIRALH 300  
Db 241 AHYIPPLTFTPVTPVTPAYWQIHMERVKVGQPLTLCKGCAAILDTGTSLLTGPIEIRALH 300

QY 301 AAIGGIPLAGEYIILCSEIPKLPAVSFLGGTMWENLTAAHDYVIIQTTNGVRCLSGFOA 360  
Db 301 AAIGGIPLAGEYIILCSEIPKLPAVSFLGGTMWENLTAAHDYVIIQTTNGVRCLSGFOA 360

QY 361 LDVPPPAGPFWILGDPVFGTYIAYFDRGMKSSARVGLARTRGADLGWGETAQAOQPG 420  
Db 361 LDVPPPAGPFWILGDPVFGTYIAYFDRGMKSSARVGLARTRGADLGWGETAQAOQPG 420

QY 374 LDVPPPAGPFWILGDPVFGTYIAYFDRGMKSSARVGLARTRGADLGWGETAQAOQPG 433  
Db 374 LDVPPPAGPFWILGDPVFGTYIAYFDRGMKSSARVGLARTRGADLGWGETAQAOQPG 433

RESULT 5  
US-10-094-080-3  
; Sequence 3, Application US/10094080  
; Publication No. US20020107140A1  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Roger  
; COLEMAN, Olga  
; TITLE OF INVENTION: TWO NOVEL HUMAN CATECHOLIN PROTEINS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: U.S.  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSEQ Version 1.5  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/094,080  
; FILING DATE: 07-Mar-2002  
; CLASSIFICATION: <Unknown>  
; PRIORITY APPLICATION DATA:  
; APPLICATION NUMBER: 09/387,413  
; FILING DATE: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Billings, Lucy J  
; REGISTRATION NUMBER: 36,749  
; REFERENCE/DOCKET NUMBER: PF-0125 US  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415-855-0555  
; TELEFAX: 415-845-4166  
; TELE: <Unknown>  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 395 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: Peptide  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; FRAGMENT TYPE: N-terminal  
; ORIGINAL SOURCE:  
; IMMEDIATE SOURCE:  
; LIBRARY: LUNGNOT02  
; CLONE: 312099  
; SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

SEQ ID NO 31  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-09-964-899-11

Query Match 99.7%; Score 2232; DB 9; Length 433;  
Best Local Similarity 99.8%; Pred. No. 7.6e-219; Indels 0; Gaps 0;  
Matches 419; Conservative 0; Mismatches 1;

QY 1 MSPPPLQLLPLNVEPSGATLIRIPLHRVQGRTRNLGRWRAEPLPKLGAPS 60  
Db 14 MSPPPLQLLPLNVEPSGATLIRIPLHRVQGRTRNLGRWRAEPLPKLGAPS 73

QY 61 PGDKP1FVPLSNYRDQYFGEIGLGTQNPNTVAFDTGSNLWPSRQHFFSVPWMUH 120  
Db 74 PGDKP1FVPLSNYRDQYFGEIGLGTQNPNTVAFDTGSNLWPSRQHFFSVPWMUH 133



Db 419 G 419

RESULT 8  
US-09-915-582-66  
Sequence 66, Application US/09915582  
Patent No. US20020120103A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 17 Human Secreted Proteins  
CURRENT APPLICATION NUMBER: US/09/915,582  
PRIOR APPLICATION NUMBER: PCT/US01/01431  
PRIOR FILING DATE: 2001-01-17  
FILE REFERENCE: PS7231  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/231,968  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 66  
LENGTH: 262  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (231)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-915-582-66

Query Match 59.3%; Score 1328; DB 11; Length 262;  
Best Local Similarity 97.6%; Pred. No. 6.2e-121;  
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 MSPPPLQPLQLLPLNVEPSGATLIRIPLHRVQGRTLNLRLWRPAELPKLGAPS 60  
Db 1 MSPPPLQPLQLLPLNVEPSGATLIRIPLHRVQGRTLNLRLWRPAELPKLGAPS 60  
Qy 61 PGDKP1FVPLSNYRDQFQANGTKFAQYGTGRDGFPLQVPPQNTVAFTGSSNLWVPSRRCFFFSVPCWLH 120  
Db 61 PGDKP1FVPLSNYRDQFQANGTKFAQYGTGRDGFPLQVPPQNTVAFTGSSNLWVPSRRCFFFSVPCWLH 120  
Qy 121 RFDPKASSSFQANGTKFAQYGTGRDGFPLQVPPQNTVAFTGSSNLWVPSRRCFFFSVPCWLH 120  
Db 121 RFDPKASSSFQANGTKFAQYGTGRDGFPLQVPPQNTVAFTGSSNLWVPSRRCFFFSVPCWLH 120  
Qy 181 AHFDGTLGLGFPLILVEVGTRPPMDVLTVEQGLLDRKVFSTLNRDPEEPDGXELVIGGSDF 240  
Db 181 AHFDGTLGLGFPLILVEVGTRPPMDVLTVEQGLLDRKVFSTLNRDPEEPDGXELVIGGSDF 240  
Qy 241 AHYIPPLTFYPTVTP 255  
Db 241 AHYIPPLTFYPTVTP 255  
Qy 241 AHYIPSPFPVVRSP 255  
Db 241 AHYIPSPFPVVRSP 255

RESULT 10  
US-10-277-802-66  
Sequence 66, Application US/10277802  
Publication No. US2003019070A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: 17 Human Secreted Proteins  
FILE REFERENCE: PS7231  
CURRENT APPLICATION NUMBER: US/10/277,802  
CURRENT FILING DATE: 2003-10-13  
PRIOR APPLICATION NUMBER: 09/315,582  
PRIOR FILING DATE: 2001-07-27  
PRIOR APPLICATION NUMBER: PCT/US01/01431  
PRIOR FILING DATE: 2001-01-17  
PRIOR APPLICATION NUMBER: 60/179,065  
PRIOR FILING DATE: 2000-01-31  
PRIOR APPLICATION NUMBER: 60/180,628  
PRIOR FILING DATE: 2000-02-04  
PRIOR APPLICATION NUMBER: 60/231,968  
PRIOR FILING DATE: 2000-09-12  
NUMBER OF SEQ ID NOS: 97  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 66  
LENGTH: 262  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (231)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-10-277-802-66

Query Match 59.3%; Score 1328; DB 14; Length 262;  
Best Local Similarity 97.6%; Pred. No. 6.2e-121;  
Matches 249; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

RESULT 9  
US-09-833-245-1469  
Sequence 1469, Application US/09833245  
Publication No. US20040010134A1  
GENERAL INFORMATION:  
APPLICANT: Human Genome Sciences, Inc.  
TITLE OF INVENTION: Albumin Fusion Proteins  
FILE REFERENCE: PF546POT  
CURRENT APPLICATION NUMBER: US/09/833,245  
CURRENT FILING DATE: 2001-04-12  
PRIOR APPLICATION NUMBER: 60/229, 358  
PRIOR FILING DATE: 2000-04-12  
PRIOR APPLICATION NUMBER: 60/256, 931  
PRIOR FILING DATE: 2000-12-21  
PRIOR APPLICATION NUMBER: 60/199, 384

Qy 1 MSPPPLQPLLLLPLINVEPSGATLIRIPIHRYOPGRTRNLRLGWRPAELPKLGAPS 60  
 Db 1 MSPPPLQPLLLLPLINVEPSGATLIRIPIHRYOPGRTRNLRLGWRPAELPKLGAPS 60  
 Qy 61 PGDKPFLVPLSMYRVDYQFGEIGLGTTPQNFTVAFDTGSNNLWPSRRCHFEFSVPCWLHH 120  
 Db 61 PGDKPFLVPLSMYRVDYQFGEIGLGTTPQNFTVAFDTGSNNLWPSRRCHFEFSVPCWLHH 120  
 Qy 121 RFDPKASSFQANGTKFAIQYGTGRDYLSEKDLTIGIGASVIFGEALWEPSLYEAF 180  
 Db 121 RFDPKASSFQANGTKFAIQYGTGRDYLSEKDLTIGIGASVIFGEALWEPSLYEAF 180  
 Qy 181 AHFDGILGLGFPLSVEGVRFPRMDFPEPDGEBLVUGLGSDF 240  
 Db 191 AHFDGILGLGFPLSVEGVRFPRMDFPEPDGEBLVUGLGSDF 240  
 Qy 241 AHYIPPLTFVPTVP 255  
 Db 241 AHYIPPLTFVPTVP 255

Qy 241 AHYIPPLTFVPTVP 255  
 Db 241 AHYIPPLTFVPTVP 255  
 RESULT 11  
 US-09-925-302-670  
 ; Sequence 670, Application US/09925302  
 ; Parental No. US20044941A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies  
 ; FILE REFERENCE: PA104  
 ; CURRENT APPLICATION NUMBER: US/09/925,302  
 ; PRIORITY APPLICATION NUMBER: PCT/US00/05918  
 ; CURRENT FILING DATE: 2001-08-10  
 ; PRIOR FILING DATE: 2000-03-08  
 ; PRIORITY NUMBER: 60/124,270  
 ; PRIORITY FILING DATE: 1999-03-12  
 ; NUMBER OF SEQ ID NOS: 896  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 670  
 ; LENGTH: 285  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-09-925-302-670

Qy 241 AHYIPPLTFVPTVP 255  
 Db 241 AHYIPPLTFVPTVP 255  
 Query Match 52.7%; Score 1179; DB 9; Length 285;  
 Best Local Similarity 80.7%; Pred. No. 2.4e-10; Indels 42; Gaps 2;  
 Matches 230; Conservative 4; Mismatches 9; InDel's 42; Gaps 2;

RESULT 12  
 US-09-925-302-670  
 ; Sequence 670, Application US/09925302  
 ; Parental No. US20044941A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 17 Human Secreted Proteins  
 ; FILE REFERENCE: PS723P1  
 ; CURRENT APPLICATION NUMBER: US/09/915,582  
 ; PRIORITY NUMBER: PCT/US01/01431  
 ; PRIORITY FILING DATE: 2001-07-27  
 ; PRIORITY NUMBER: 60/1179,065  
 ; PRIORITY FILING DATE: 2000-01-31  
 ; PRIORITY NUMBER: 60/180,628  
 ; PRIORITY FILING DATE: 2000-02-04  
 ; PRIORITY NUMBER: 60/231,968  
 ; PRIORITY FILING DATE: 2000-09-12  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 670  
 ; LENGTH: 212  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (9)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

Qy 141 YGTCRVDGILSLEDKLTTIGIGKASVIFGEALWEPSLYAFAAHFDGILGLGFPLSVEGVR 200  
 Db 121 YGTCRVHGILSLEDKLTTIGIGKASVIFGEALWEPSLYAFAAHFDGILGLGFPLSVEGVR 180  
 Qy 201 PPMDVVLVEGGLDKEPKVFSYLNRDPEEPDGGEVLVGGSDPAHYIPLTFVPTVPAYQI 260  
 Db 181 PPMDVVLVEGGLDKEPKVFSYLNRDPEEPDGGEVLVGGSDPAHYIPLTFVPTVPAYQI 240  
 Qy 261 HMERVKVGPGTLCAKGCAAIDTGSLLITOPTERIALHAAGG 305  
 Db 241 HMERVKVGPGTLCAKGCAAIDTGSLLITOPTERIALHAAGG 285  
 ; RESULT 13  
 ; US-09-915-582-87  
 ; Sequence 87, Application US/09915582  
 ; Parental No. US20020120103A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 17 Human Secreted Proteins  
 ; FILE REFERENCE: PS723P1  
 ; CURRENT APPLICATION NUMBER: US/09/915,582  
 ; PRIORITY NUMBER: PCT/US01/01431  
 ; PRIORITY FILING DATE: 2001-07-27  
 ; PRIORITY NUMBER: 60/1179,065  
 ; PRIORITY FILING DATE: 2000-01-31  
 ; PRIORITY NUMBER: 60/180,628  
 ; PRIORITY FILING DATE: 2000-02-04  
 ; PRIORITY NUMBER: 60/231,968  
 ; PRIORITY FILING DATE: 2000-09-12  
 ; NUMBER OF SEQ ID NOS: 97  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO: 87  
 ; LENGTH: 212  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (9)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

RESULT 12  
 US-09-925-302-670  
 ; Sequence 670, Application US/09925302  
 ; Publication No. US20030064072A9

Query Match 46.9%; Score 1050; DB 9; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-94; Indels 0; Gaps 0;  
 Matches 197; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 224 DPEEPDGELVLGGSDPAHYIPPLTFVPTVPAWQIHMERVKVGPGILTCAKGCAAILD 283  
 Db 16 DPEEPDGELVLGGSDPAHYIPPLTFVPTVPAWQIHMERVKVGPGILTCAKGCAAILD 75

QY 284 TGTSLITGPTEIRALHAAGGIPILLAGEXYLICSEIPIKUPAYSFLIGGWENFTAHDYV 343  
 Db 76 TGTSLITGPTEIRALHAAGGIPILLAGEXYLICSEIPIKUPAYSFLIGGWENFTAHDYV 135

QY 344 IQTTRNGVRICLGSFQALDYPAPPFWILGDVFLTGTYAVEDRGDMKSSARVGLARART 403  
 Db 136 IQTTRNGVRICLGSFQALDYPAPPFWILGDVFLTGTYAVEDRGDMKSSARVGLARART 195

QY 404 RGADLGWGETAQAFPG 420  
 Db 196 RGADLGWGETAQAFPG 212

RESULT 14  
 US-09-833-245-1471  
 ; Sequence 14/1, Application US/09833245  
 ; Publication No. US2004010134A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Human Genome Sciences, Inc.  
 ; TITLE OF INVENTION: Albumin Fusion Proteins  
 ; FILE REFERENCE: PF546PCT  
 ; CURRENT APPLICATION NUMBER: US/09/833, 245  
 ; PRIORITY NUMBER: 60/229, 358  
 ; PRIOR FILING DATE: 2000-04-12  
 ; PRIORITY NUMBER: 60/256, 931  
 ; PRIOR FILING DATE: 2000-12-21  
 ; PRIORITY NUMBER: 60/199, 384  
 ; PRIOR FILING DATE: 2000-04-25  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO: 87  
 ; LENGTH: 212  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (9)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 US-10-277-802-87

Query Match 46.9%; Score 1050; DB 14; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-94; Indels 0; Gaps 0;

QY 224 DPERRPDGGFLVLSGSDPAHYIPPLTFVPTVPAWQIHMERVKVGPGILTCAKGCAAILD 283  
 Db 16 DPERRPDGGFLVLSGSDPAHYIPPLTFVPTVPAWQIHMERVKVGPGILTCAKGCAAILD 75

QY 284 TGTSLITGPTEIRALHAAGGIPILLAGEXYLICSEIPIKUPAYSFLIGGWENFTAHDYV 343  
 Db 76 TGTSLITGPTEIRALHAAGGIPILLAGEXYLICSEIPIKUPAYSFLIGGWENFTAHDYV 135

QY 344 IQTTRNGVRICLGSFQALDYPAPPFWILGDVFLTGTYAVEDRGDMKSSARVGLARART 403  
 Db 136 IQTTRNGVRICLGSFQALDYPAPPFWILGDVFLTGTYAVEDRGDMKSSARVGLARART 195

QY 404 RGADLGWGETAQAFPG 420  
 Db 196 RGADLGWGETAQAFPG 212

Search completed: June 2, 2004, 20:25:19  
 Job time : 75.8784 secs

Query Match 46.9%; Score 1050; DB 11; Length 212;  
 Best Local Similarity 100.0%; Pred. No. 6.2e-94; Indels 0; Gaps 0;

QY 224 DPEEPDGELVLGGSDPAHYIPPLTFVPTVPAWQIHMERVKVGPGILTCAKGCAAILD 283  
 Db 16 DPEEPDGELVLGGSDPAHYIPPLTFVPTVPAWQIHMERVKVGPGILTCAKGCAAILD 75

QY 284 TGTSLITGPTEIRALHAAGGIPILLAGEXYLICSEIPIKUPAYSFLIGGWENFTAHDYV 343  
 Db 76 TGTSLITGPTEIRALHAAGGIPILLAGEXYLICSEIPIKUPAYSFLIGGWENFTAHDYV 135

QY 344 IQTTRNGVRICLGSFQALDYPAPPFWILGDVFLTGTYAVEDRGDMKSSARVGLARART 403  
 Db 136 IQTTRNGVRICLGSFQALDYPAPPFWILGDVFLTGTYAVEDRGDMKSSARVGLARART 195

QY 404 RGADLGWGETAQAFPG 420  
 Db 196 RGADLGWGETAQAFPG 212

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## OM protein - protein search, using sw model.

Run on: June 2, 2004, 20:16:40 ; Search time 29.2707 Seconds

740.773 Million cell updates/sec  
 (without alignments)Title: US-09-700-770-8  
 Perfect score: 2238

Sequence: 1 MSPPPLQPHILLPLNVE.....ARTRGADLGWGETAQQPPG 420

Scoring table: BLOSUM62  
 Gapext 10.0 , Gapop 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters:

389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents MA:\*

1: /cgn2\_6/.ptodata/2/iaa/5A\_COMB.pep:\*
 2: /cgn2\_6/.ptodata/2/iaa/5B\_COMB.pep:\*
 3: /cgn2\_6/.ptodata/2/iaa/6A\_COMB.pep:\*
 4: /cgn2\_6/.ptodata/2/iaa/6B\_COMB.pep:\*
 5: /cgn2\_6/.ptodata/2/iaa/FACTUS\_COMB.pep:\*
 6: /cgn2\_6/.ptodata/2/iaa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2238	100.0	420	3	US-09-008-271A-4	Sequence 4, Appli
2	2238	100.0	420	4	US-09-705-448-1	Sequence 1, Appli
3	2238	99.7	420	3	US-08-974-691-6	Sequence 8, Appli
4	2069.5	92.5	395	1	US-08-723-938-3	Sequence 3, Appli
5	2069.5	92.5	395	2	US-09-080-538-3	Sequence 3, Appli
6	2069.5	92.5	395	4	US-03-387-413-3	Sequence 12, Appli
7	1897	84.8	445	3	US-08-974-691-6	Sequence 6, Appli
8	1897	84.8	451	3	US-08-974-691-2	Sequence 2, Appli
9	1897	83.9	433	4	US-09-705-448-3	Sequence 3, Appli
10	1564.5	69.9	419	3	US-08-974-691-3	Sequence 3, Appli
11	1560.5	69.7	419	4	US-09-705-448-10	Sequence 10, Appli
12	1015	45.4	412	1	US-08-208-007A-12	Sequence 12, Appli
13	1015	45.4	412	3	US-08-974-691-4	Sequence 4, Appli
14	1015	45.4	412	4	US-08-915-095A-12	Sequence 12, Appli
15	1015	45.4	412	4	US-08-798-095A-12	Sequence 12, Appli
16	1015	45.4	412	4	US-08-798-095A-12	Sequence 12, Appli
17	1015	45.4	412	4	US-09-953-956-12	Sequence 12, Appli
18	1015	45.4	412	4	US-08-153-125A-12	Sequence 12, Appli
19	1015	45.4	412	4	US-09-215-450-25	Sequence 25, Appli
20	1015	45.4	412	4	US-10-114-464-12	Sequence 12, Appli
21	869	38.8	396	1	US-08-208-007A-13	Sequence 9, Appli
22	869	38.8	396	3	US-09-032-523-9	Sequence 13, Appli
23	869	38.8	396	4	US-08-915-095A-13	Sequence 13, Appli
24	869	38.8	396	4	US-08-798-095A-13	Sequence 13, Appli
25	869	38.8	396	4	US-08-953-956-13	Sequence 13, Appli
26	869	38.8	396	4	US-08-553-125A-13	Sequence 13, Appli
27	869	38.8	396	4	US-08-553-125A-13	Sequence 13, Appli

## ALIGNMENTS

RESULT 1  
 US-09-008-271A-4  
 ; Sequence 4, Application US/09008271A  
 ; Patent No. 6203979  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; Hillman, Jennifer L.  
 ; Yue, Henry  
 ; Guegler, Karl J.  
 ; Corley, Neil C.  
 ; Tang, Tom Y.  
 ; Shah, Purvi  
 ; TITLE OF INVENTION: HUMAN PROTEASE MOLECULES  
 ; NUMBER OF SEQUENCES: 24  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Dr.  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: USA  
 ; ZIP: 94104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FASTSEQ FOR Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/008,271A.  
 ; FILING DATE: 16-Jan-1998  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: <Unknown>  
 ; FILING DATE: <Unknown>  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Mohan-Peterson, Sheila  
 ; REGISTRATION NUMBER: 41,201  
 ; TELECOMMUNICATION INFORMATION:  
 ; APPLICATION NUMBER: PP-0458 US  
 ; FILING DATE: 16-Jan-1998  
 ; TELEPHONE: 650-855-0555  
 ; TELEFAX: 650-845-4166  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 420 amino acids  
 ; TYPE: amino acid  
 ; STRANDBEDNESS: Single  
 ; TOPOLOGY: linear  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: LUNGAST01  
 ; CLONE: 877617  
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

US-09-008-271A-4

Page 2

Query Match 99.7%; Score 2232; DB 3; Length 420;  
 Best Local Similarity 99.8%; Pred. No. 8.5e-222;  
 Matches 419; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPPPLQLPILLPLNVEPSGATLIRIPLHRYQPGRBTNLNLRGWRPAELPKLGAPS 60  
 Db 1 MSPPPLQLPILLPLNVEPSGATLIRIPLHRYQPGRBTNLNLRGWRPAELPKLGAPS 60

Qy 61 PGDKPIFVPLSNYTFDVOYQEIGIGTPQNFTVAFDTGSNLWPSRCHFFSVPWCMLHH 120  
 Db 61 PGDKPIFVPLSNYTFDVOYQEIGIGTPQNFTVAFDTGSNLWPSRCHFFSVPWCMLHH 120

Qy 121 RFDPKASSQFQANGTKFAIQCGRDVGILSEDKLITGIGKASVIFGIGALWERSLVEAF 180  
 Db 121 RFDPKASSQFQANGTKFAIQCGRDVGILSEDKLITGIGKASVIFGIGALWERSLVEAF 180

Qy 181 AHFDGILGLGFPLSVEGTRPMPDVLYVEQFLDKPVFSSTYLNRDPEEPGGELVLGGSDP 240  
 Db 181 AHFDGILGLGFPLSVEGTRPMPDVLYVEQFLDKPVFSSTYLNRDPEEPGGELVLGGSDP 240

Qy 241 AHYIPPLTIVPTVTPAYQTHMERYVKVGLPOLTCAGCAGAILDTGTSLLITGPTEIRALH 300  
 Db 241 AHYIPPLTIVPTVTPAYQTHMERYVKVGLPOLTCAGCAGAILDTGTSLLITGPTEIRALH 300

Qy 301 AAIGGIPLAGEYIILCSEPKLPAVSFLIGGWENLTADHYVQTTRANGVRCLSGFPA 360  
 Db 301 AAIGGIPLAGEYIILCSEPKLPAVSFLIGGWENLTADHYVQTTRANGVRCLSGFPA 360

Qy 361 LDVPPPAGFWILGDFVFLGTIVAYVAFDRGDMKSSARVGLARARTGADLGWGETAQAOFG 420  
 Db 361 LDVPPPAGFWILGDFVFLGTIVAYVAFDRGDMKSSARVGLARARTGADLGWGETAQAOFG 420

RESULT 4  
 US-08-723-938-3  
 Sequence 3, Application US/08723938  
 Patent No. 5776759

GENERAL INFORMATION:  
 APPLICANT: Bandman, Olga  
 APPLICANT: Coleman, Roger  
 TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS  
 NUMBER OF SEQUENCES: 4  
 CURRENT APPLICATION ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/723,938  
 FILING DATE:  
 CLASSIFICATION: 530  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PP-0125 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 395 amino acids

TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 HYPOTHETICAL: NO  
 ANTI-SENSE: NO  
 FRAGMENT TYPE: N-terminal  
 IMMEDIATE SOURCE:  
 LIBRARY: LUNGNOTO2  
 CLONE: 312099  
 US-08-723-938-3

Query Match 92.5%; Score 2069.5; DB 1;  
 Best Local Similarity 93.8%; Prod. No. 4.6e-205;  
 Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

Qy 1 MSPPPLQLPILLPLNVEPSGATLIRIPLHRYQPGRBTNLNLRGWRPAELPKLGAPS 60  
 Db 1 MSPPPLQLPILLPLNVEPSGATLIRIPLHRYQPGRBTNLNLRGWRPAELPKLGAPS 60

Qy 61 PGDKPIFVPLSNYTFDVOYQEIGIGTPQNFTVAFDTGSNLWPSRCHFFSVPWCMLHH 120  
 Db 61 PGDKPIFVPLSNYTFDVOYQEIGIGTPQNFTVAFDTGSNLWPSRCHFFSVPWCMLHH 120

Qy 121 RFDPKASSQFQANGTKFAIQCGRDVGILSEDKLITGIGKASVIFGIGALWERSLVEAF 180  
 Db 121 RFDPKASSQFQANGTKFAIQCGRDVGILSEDKLITGIGKASVIFGIGALWERSLVEAF 180

Qy 181 AHFDGILGLGFPLSVEGTRPMPDVLYVEQFLDKPVFSSTYLNRDPEEPGGELVLGGSDP 240  
 Db 181 AHFDGILGLGFPLSVEGTRPMPDVLYVEQFLDKPVFSSTYLNRDPEEPGGELVLGGSDP 240

Qy 241 AHYIPPLTIVPTVTPAYQTHMERYVKVGLPOLTCAGCAGAILDTGTSLLITGPTEIRALH 300  
 Db 241 AHYIPPLTIVPTVTPAYQTHMERYVKVGLPOLTCAGCAGAILDTGTSLLITGPTEIRALH 300

Qy 301 AAIGGIPLAGEYIILCSEPKLPAVSFLIGGWENLTADHYVQTTRANGVRCLSGFPA 360  
 Db 301 AAIGGIPLAGEYIILCSEPKLPAVSFLIGGWENLTADHYVQTTRANGVRCLSGFPA 360

Qy 361 LDVPPPAGFWILGDFVFLGTIVAYVAFDRGDMKSSARVGLARARTGADLGWGETAQAOFG 420  
 Db 361 LDVPPPAGFWILGDFVFLGTIVAYVAFDRGDMKSSARVGLARARTGADLGWGETAQAOFG 420

RESULT 5  
 US-09-08-538-3  
 Sequence 3, Application US/09080538  
 Patent No. 5965129

GENERAL INFORMATION:  
 APPLICANT: Bandman, Olga  
 APPLICANT: Coleman, Roger  
 TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.  
 ZIP: 94304

COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FastSSQ Version 1.5  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/080,538  
 FILING DATE:  
 CLASSIFICATION:  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PP-0125 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEX: 415-845-4166  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 395 amino acids

FILING DATE: ZIP: 94304  
 ATTORNEY/AGENT INFORMATION: COMPUTER READABLE FORM:  
 NAME: Billings, Lucy J MEDIUM TYPE: Diskette  
 REGISTRATION NUMBER: 36,749 COMPUTER: IBM Compatible  
 TELECOMMUNICATION INFORMATION: OPERATING SYSTEM: DOS  
 TELEPHONE: 415-855-0555 SOFTWARE: FastSEQ Version 1.5  
 TELEFAX: 415-845-4166 CURRENT APPLICATION DATA:  
 FILING DATE: 31-Aug-1999  
 CLASSIFICATION: <Unknown>  
 PRIORITY DATA: APPLICATION NUMBER: 09/080,538  
 PRIORITY NUMBER: <Unknown>  
 PRIORITY DATE: <Unknown>  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Billings, Lucy J  
 REGISTRATION NUMBER: 36,749  
 REFERENCE/DOCKET NUMBER: PF-0125 US  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-855-0555  
 TELEFAX: 415-845-4166  
 TELEX: <Unknown>  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 395 amino acids  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: Peptide  
 HYPOTHETICAL: No  
 ANTI-SENSE: No  
 FRAGMENT TYPE: N-terminal  
 ORIGINAL SOURCE:  
 IMMEDIATE SOURCE:  
 LIBRARY: LUNGNOT02  
 CLONE: 312099  
 SEQUENCE DESCRIPTION: SEQ ID NO: 3:  
 US-09-080-538-3

Query Match Score 2069.5%; DB 2; Length 395;  
 Best Local Similarity 93.8%; Pred. No. 4.6e-205;  
 Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

Qy 1 MSPPPLIQLPILLPLINVEPSGATLIRIPLHRVQPERALPKLGAPS 60  
 Db 1 MSPPPLIQLPILLPLINVEPSGATLIRIPLHRVQPERALPKLGAPS 60

Qy 61 PGDKPFLVPLSNYRDYQFGEGLGTPPQNFTVIAFDTGSSNWVPSRRCHFSPVPLHH 120  
 Db 61 PGDKPFLVPLSNYRDYQFGEGLGTPPQNFTVIAFDTGSSNWVPSRRCHFSPVPLHH 120

Qy 121 RFPDKASSFQANGTKPAIQGTGRNDGILSDEKLTIGIGKASVTFGEALWEPSPLYPAF 180  
 Db 121 RFPDKASSFQANGTKPAIQGTGRNDGILSDEKLTIGIGKASVTFGEALWEPSPLYPAF 180

Qy 181 AHFDGILGLGFPLISVEGVRPPMDVLYQGLIDKPVSFYLNRDPEEPDGELVLGGSDP 240  
 Db 181 AHFDGILGLGFPLISVEGVRPPMDVLYQGLIDKPVSFYLNRDPEEPDGELVLGGSDP 240

Qy 241 AHYIPPLTFVPTVPAWQIHMERVKPVGTLCKGCAAILDTGTSLITCPTEETRALH 300  
 Db 241 AHYIPPLTFVPTVPAWQIHMERVKPVGTLCKGCAAILDTGTSLITCPTEETRALH 300

Qy 301 AAGGIPPLAGETILCSB1KLPAYSFLGGWFMNTAHDYVCTTRNGYRLCLSGFQA 360  
 Db 301 AAGGIPPLAGETILCSB1KLPAYSFLGGWFMNTAHDYVCTTRNGYRLCLSGFQA 360

Qy 341 LDVPPPGFPFWLGDYFVLTGKQVPLKAVDQCDMKSSARVGLARTRGADLGKGETAQQPG 420  
 Db 350 -----DVFHTGTYAVFDQCDMKSSARVGLARTRGADLGKGETAQQPG 395

RESULT 6  
 US-09-387-413-3  
 Sequence 3, Application US/09387413  
 Patent No. 6475485  
 GENERAL INFORMATION:  
 APPLICANT: Bandman, Oleg  
 Coleman, Roger  
 TITLE OF INVENTION: TWO NOVEL HUMAN CATHESPIN PROTEINS  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 STREET: 3174 Porter Drive  
 CITY: Palo Alto  
 STATE: CA  
 COUNTRY: U.S.

RESULT 7  
 US-08-974-691-6

Sequence 6, Application US/08974691  
 Patent No. 6225103  
 GENERAL INFORMATION:  
 APPLICANT: Keisch, Gerald  
 APPLICANT: Lin, Xinli  
 APPLICANT: Tang, Jordan  
 TITLE OF INVENTION: Cloning and Characterization of Napsin  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Patrea L. Pabst  
 STREET: 2800 One Atlantic Center, 1201 W. Peachtree  
 CITY: Atlanta  
 STATE: GA  
 COUNTRY: USA  
 ZIP: 30309-3450  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/974,691  
 FILING DATE: 20-NOV-1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/0031/196  
 FILING DATE: 20-NOV-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US/046,126  
 FILING DATE: 09-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Pabst, Patrea L.  
 REGISTRATION NUMBER: 31,284  
 REFERENCE/DOCKET NUMBER: OMRF 166  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 404-873-8794  
 TELEFAX: 404-873-8795  
 SEQUENCE CHARACTERISTICS:  
 FOR SEQ ID NO: 6 :  
 LENGTH: 445 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-08-974-691-6

Query Match 84.8%; Score 1897; DB 3; Length 445;  
 Best Local Similarity 86.0%; Pred. No. 3.5e-187;  
 Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MSPPPLQLPILLPLPLNVEPSGATLIRIPLHRYQPGRTLNLRGWRPAELPKLGARS 60  
 Db 1 MSPPPLQLPILLPLPLNVEPSGATLIRIPLHRYQPGRTLNLRGWRPAELPKLGARS 60

Qy 61 PGDKPLFVPLSNYDVOYGEIGTPONFTYAPDTGSSNLWYPSRCHFEFSYPCMLHH 120  
 Db 61 PGDKPLFVPLSNYDVOYGEIGTPONFTYAPDTGSSNLWYPSRCHFEFSYPCMLHH 120

Qy 121 RFDPKASSQOANGTKFAIQYGTGRDVGLLSEDKLTTGGIKGASVIFGEALWESSLVFTV 180  
 Db 121 RFNPMASSFXPSGTMKFAIQYGTGRDVGLLSEDKLTTGGIKGASVIFGEALWESSLVFTV 180

Qy 181 AHFDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240  
 Db 181 SRPDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240

Qy 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300  
 Db 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300

Qy 301 AAIGGIPPLAGYILCSEIPKLPAVSFLGGYWFNUITAHDYVQTTRNGYRLCLSGFOA 360  
 Db 301 AAIGGIPPLAGYILCSEIPKLPAVSFLGGYWFNUITAHDYVQTTRNGYRLCLSGFOA 360  
 Qy 361 LDVPPPAGEPFWLGDVFGLGTYAVFDRDMKSARVGLARTRGADLGWTAAQOPGP 420  
 Db 361 LDIASPPVWVILGDVFGLGTYAVFDRDMKSARVGLARTRGADLGWTAAQOPGP 420

RESULT 8  
 US-08-974-691-2  
 ; Sequence 2, Application US/08974691  
 ; Patent No. 6225103  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keisch, Gerald  
 ; APPLICANT: Lin, Xinli  
 ; APPLICANT: Tang, Jordan and Characterization of Napsin  
 ; TITLE OF INVENTION: Cloning and Characterization of Napsin  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Patrea L. Pabst  
 ; STREET: 2800 One Atlantic Center, 1201 W. Peachtree  
 ; CITY: St. St.  
 ; STATE: GA  
 ; COUNTRY: USA  
 ; ZIP: 30309-3450  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/974,691  
 ; FILING DATE: 20-NOV-1997  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/0031/196  
 ; FILING DATE: 20-NOV-1996  
 ; PRIORITY APPLICATION DATA:  
 ; APPLICATION NUMBER: US/046,126  
 ; FILING DATE: 09-MAY-1997  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Pabst, Patrea L.  
 ; REGISTRATION NUMBER: 31,284  
 ; REFERENCE/DOCKET NUMBER: OMRF 166  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 404-873-8794  
 ; TELEFAX: 404-873-8795  
 ; SEQUENCE CHARACTERISTICS:  
 ; FOR SEQ ID NO: 6 :  
 ; LENGTH: 445 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; ORIGINAL SOURCE:  
 ; ORGANISM: Homo sapiens  
 ; US-08-974-691-2

Query Match 84.8%; Score 1897; DB 3; Length 451;  
 Best Local Similarity 86.0%; Pred. No. 3.3e-187;  
 Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MSPPPLQLPILLPLPLNVEPSGATLIRIPLHRYQPGRTLNLRGWRPAELPKLGAPS 60  
 Db 1 MSPPPLQLPILLPLPLNVEPSGATLIRIPLHRYQPGRTLNLRGWRPAELPKLGAPS 60

Qy 61 PGDKPLFVPLSNYDVOYGEIGTPONFTYAPDTGSSNLWYPSRCHFEFSYPCMLHH 120  
 Db 61 PGDKPLFVPLSNYDVOYGEIGTPONFTYAPDTGSSNLWYPSRCHFEFSYPCMLHH 120

Qy 181 AHFDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240  
 Db 181 SRPDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240

Qy 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300  
 Db 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300

Qy 121 RFDPKASSQOANGTKFAIQYGTGRDVGLLSEDKLTTGGIKGASVIFGEALWESSLVFTV 180  
 Db 121 RFNPMASSFXPSGTMKFAIQYGTGRDVGLLSEDKLTTGGIKGASVIFGEALWESSLVFTV 180

Qy 181 AHFDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240  
 Db 181 SRPDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240

Qy 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300  
 Db 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300

Qy 121 RFDPKASSQOANGTKFAIQYGTGRDVGLLSEDKLTTGGIKGASVIFGEALWESSLVFTV 180  
 Db 121 RFNPMASSFXPSGTMKFAIQYGTGRDVGLLSEDKLTTGGIKGASVIFGEALWESSLVFTV 180

Qy 181 AHFDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240  
 Db 181 SRPDGILGLGPILSYVGPPMDVLYEGQDLPPEPDGELMVLGGSDP 240

Qy 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300  
 Db 241 AHYIPPLTFVPTVTPAYWQIHMERVKVGPGLTCAHGCAAILDTSLTGPTETIRALH 300

RESULT 9  
US-09-705-448-3  
 / Sequence 3, Application US/09705448  
 / GENERAL INFORMATION:  
 / APPLICANT: Xu, Hong  
 / APPLICANT: Bruno, Sandra A.  
 / APPLICANT: Elsenboss, Laura A.  
 / APPLICANT: Fogliano, Michael  
 / APPLICANT: Cohan, Victoria L.  
 / APPLICANT: Bandman, Olga  
 / TITLE OF INVENTION: HUMAN ASPARTIC PROTEASES  
 / FILE REFERENCE: PF-0458-1.CIP  
 / CURRENT APPLICATION NUMBER: US/09/705,448  
 / CURRENT FILING DATE: 2000-11-02  
 / PRIOR APPLICATION NUMBER: 09/116,641  
 / PRIOR FILING DATE: 1998-07-16  
 / PRIOR APPLICATION NUMBER: 09/009,271  
 / PRIOR FILING DATE: 1998-01-16  
 / NUMBER OF SEQ ID NOS: 10  
 / SOFTWARE: FastSEQ for Windows Version 3.0  
 / SEQ ID NO: 3  
 / LENGTH: 433  
 / TYPE: PRT  
 / ORGANISM: HOMO SAPIENS  
 / FEATURE:  
 / NAME/KEY: unsure  
 / LOCATION: 322  
 / OTHER INFORMATION: 2435410, EOSTINOT03  
 / US-09-705-448-3

Query Match 83.9%; Score 1877; DB 4; Length 433;  
 Best Local Similarity 95.2%; Pred. No. 4e-185; Mismatches 17; Indels 0; Gaps 0;  
 Matches 358; Conservative 322

Db 121 RENPNASSSEKPSGKFAIQGTRGDGLLSEDKLITGGAKGASVIFGAALWESSLVFTV 180  
 Qy 181 AHFDGILGLGFPLISVEGRPMDFYDVEQQLDKEFVSTYLNDRDEPQDGELYLGSSDP 240  
 Db 181 SRPDGILGLGFPLISVEGRPMDFYDVEQQLDKEFVSTYLNDRDEPQDGELYLGSSDP 240  
 Qy 241 AHYIPLTFLFPTVTPAYQWQHMERVKPGPLTCRAKGCAAILDTGTSLITGTPTEEIRALH 300  
 Db 241 AHYIPLTFLFPTVTPAYQWQHMERVKPGPLTCRAKGCAAILDTGTSLITGTPTEEIRALH 300  
 Qy 301 AAIGGIPPLAGEYIIICSETPKLPAVSFLIGGWNFLTAHDYVQTTTRNGVRLCISGFOA 360  
 Db 301 AAIGGIPPLAGEYIIICSETPKLPAVSFLIGGWNFLTAHDYVQTTTRNGVRLCISGFOA 360  
 Qy 361 LDVPPAGFPFWLGDVEFGTYVAFDGDMKSSARVGHALARTRGADLGWGSTAQQPG 420  
 Db 361 LDASPPVWILGDVEGAYTVFDRGMKSARVGHALARTRGADLGWGSTAQQPG 420  
 Result 10  
US-08-974-691-3  
 / Sequence 3, Application US/08974691  
 / Patent No. 6225103  
 / GENERAL INFORMATION:  
 / APPLICANT: Keisch, Gerald  
 / APPLICANT: Lin, Xinli  
 / APPLICANT: Tang, Jordan  
 / TITLE OF INVENTION: Cloning and Characterization of Napsin  
 / NUMBER OF SEQUENCES: 14  
 / CORRESPONDENCE ADDRESS:  
 / ADDRESSEE: Patrea L. Pabst  
 / STREET: 2830 One Atlantic Center, 1201 W. Peachtree  
 / CITY: Atlanta  
 / STATE: GA  
 / COUNTRY: USA  
 / ZIP: 30309-3450  
 / COMPUTER READABLE FORM:  
 / MEDIUM TYPE: Floppy disk  
 / COMPUTER: IBM PC compatible  
 / OPERATING SYSTEM: PC-DOS/MS-DOS  
 / SOFTWARE: PatentIn Release #1.0, Version #1.25  
 / CURRENT APPLICATION NUMBER: US/08/974,691  
 / FILING DATE: 20-NOV-1997  
 / CLASSIFICATION:  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/031,196  
 / FILING DATE: 20-NOV-1996  
 / PRIOR APPLICATION DATA:  
 / APPLICATION NUMBER: US 60/046,126  
 / FILING DATE: 09-MAY-1997  
 / ATTORNEY/AGENT INFORMATION:  
 / NAME: Pabst, Patrea L.  
 / REGISTRATION NUMBER: 31,284  
 / REFERENCE/DOCKET NUMBER: OMRF 166  
 / TELECOMMUNICATION INFORMATION:  
 / TELEPHONE: 404-873-8794  
 / TELEFAX: 404-873-8795  
 / INFORMATION FOR SEQ ID NO: 3:  
 / SEQUENCE CHARACTERISTICS:  
 / LENGTH: 419 amino acids  
 / TYPE: amino acid  
 / STRANDEDNESS: single  
 / TOPOLOGY: linear  
 / MOLECULE TYPE: protein  
 / US-08-974-691-3

Query Match 69.9%; Score 1564.5; DB 3; Length 419;  
 Best Local Similarity 70.5%; Pred. No. 6.8e-153; Mismatches 79; Indels 9; Gaps 3;  
 Matches 297; Conservative 36; MisMatches 79; DelIndel 9; Gaps 3;

Db 7 LQPLILLLPLI--NVEPGATLIRIPLHRVQPRGRTNLNRGWREPAELPKLGAPS 60  
 Qy 1 MSPLILLLPLIPLNVEPGATLIRIPLHRVQPRGRTNLNRGWREPAELPKLGAPS 60  
 Db 1 MSPLILLLPLIPLNVEPGATLIRIPLHRVQPRGRTNLNRGWREPAELPKLGAPS 60  
 Qy 121 RFDPKASSSFQANGTKPEAQYGTGRDQGILSEDKLITGGAKGASVIFGAALWESSLVFTV 180  
 Db 121 RENPNASSSEKPSGKFAIQGTRGDGLLSEDKLITGGAKGASVIFGAALWESSLVFTV 180  
 Qy 181 AHFDGILGLGFPLISVEGRPMDFYDVEQQLDKEFVSTYLNDRDEPQDGELYLGSSDP 240  
 Db 181 SRPDGILGLGFPLISVEGRPMDFYDVEQQLDKEFVSTYLNDRDEPQDGELYLGSSDP 240  
 Qy 241 AHYIPLTFLFPTVTPAYQWQHMERVKPGPLTCRAKGCAAILDTGTSLITGTPTEEIRALH 300  
 Qy 124 PKASSSPQANGTKPEAQYGTGRDGLLSEDKLITGGAKGASVIFGAALWESSLVFAAHF 183

RESULT 11  
 US-09-705-448-10  
 i Sequence 10, Application US/09705448  
 i GENERAL INFORMATION:  
 i i APPLICANT: Xu, Hong  
 i i APPLICANT: Bruno, Sandra A.  
 i i APPLICANT: Elenboss, Laura A.  
 i i APPLICANT: Fogliani, Michael  
 i i APPLICANT: Cohan, Victoria L.  
 i i APPLICANT: Bandman, Olga  
 i TITLE OF INVENTION: HUMAN ASPARTIC PROPTASES  
 i FILE REFERENCE: PP-0458-1 CIP  
 i CURRENT APPLICATION NUMBER: US/09/705,448  
 i CURRENT FILING DATE: 2000-11-02  
 i PRIORITY NUMBER: 09/116,641  
 i PRIORITY FILING DATE: 1998-07-16  
 i PRIORITY NUMBER: 09/008,271  
 i PRIORITY FILING DATE: 1998-01-16  
 i NUMBER OF SEQ ID NOS: 10  
 i SOFTWARE: FastSEQ for Windows Version 3.0  
 i SEQ ID NO: 1.0  
 i LENGTH: 419  
 i TYPE: PRT  
 i ORGANISM: MUS MUSCULUS  
 i FEATURE:  
 i OTHER INFORMATION: 1906810, GenBank  
 i  
 i US-09-705-448-10

Query Match 69.7%; Score 1560.5; DB 4; Length 419;  
 Best Local Similarity 70.3%; Pred. No. 1.8e-119;  
 Matches 296; Conservative 37; Mismatches 79; Indels 9; Gaps 3;

Qy 7 LPLLPLPLL--NVEPSEATLIRPLRVPGEERTNLGRREPAEPLPKLGAPSPE 63  
 Db 1 MSPLLPLLCLLGLNLPEAKLIRPLRVPGEERTNLGRREPAEPLPKLGAPSPE 63

Query Match 45.4%; Score 1015; DB 1; Length 412;  
 Best Local Similarity 46.9%; Pred. No. 3.5e-96;  
 Matches 196; Conservative 71; Mismatches 123; Indel 18 26; Gaps 5;

Qy 1 MSPPPLQPLPLLPLLPNVEPSGATLIRPLRVPGRRTNLGRRE------PAELP 54  
 Db 1 MQPSSLPLACLL---AAPASA-LVPLHKEFTSIRTMSVGSEVSDLTAKPVSKY 55

Query Match 55 KLGAPSPLGPDKPFLPLSNRFDVQFGEGLGTSPQNFTVAFDTGSNHWPSRCHFFSV 114  
 Db 56 SQAVPAVTEGPIPEVLRNMYDAQYYGEIGITPPQCFTVFDTGSNHWPSTHCKLDI 115

RESULT 12  
 US-08-208-007A-12  
 i Sequence 12, Application US/08208007A  
 i Patent No. 5501969  
 i GENERAL INFORMATION:  
 i i APPLICANT: HASTINGS, ET AL.  
 i i TITLE OF INVENTION: Human Osteoclast-Derived Cathepsin  
 i i NUMBER OF SEQUENCES: 14  
 i i CORRESPONDENCE ADDRESS:  
 i i ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 i i STREET: 6 BECKER FARM ROAD  
 i i CITY: ROBBLAND  
 i i STATE: NEW JERSEY  
 i i COUNTRY: USA  
 i i ZIP: 07068  
 i i COMPUTER READABLE FORM:  
 i i MEDIUM TYPE: 3.5 INCH DISKETTE  
 i i COMPUTER: IBM PS/2  
 i i OPERATING SYSTEM: MS-DOS  
 i i SOFTWARE: WORD PERFECT 5.1  
 i i CURRENT APPLICATION DATA:  
 i i APPLICATION NUMBER: US/08/208,007A  
 i i FILING DATE: March 9, 1994  
 i i CLASSIFICATION: 435  
 i i PRIOR APPLICATION DATA:  
 i i APPLICATION NUMBER: No. 5501969e  
 i i FILING DATE: No. 5501969e  
 i i ATTORNEY/AGENT INFORMATION:  
 i i NAME: FERRARO, GREGORY D.  
 i i REGISTRATION NUMBER: 36,134  
 i i REFERENCE DOCKET NUMBER: 325800-95  
 i i TELECOMMUNICATION INFORMATION:  
 i i TELEPHONE: 201-994-1700  
 i i TELEFAX: 201-994-1744  
 i i INFORMATION FOR SEQ ID NO: 12:  
 i i SEQUENCE CHARACTERISTICS:  
 i i LENGTH: 412 AMINO ACIDS  
 i i TYPE: AMINO ACID  
 i i STRANDEDNESS:  
 i i TOPOLOGY: LINEAR  
 i i MOLECULAR TYPE: PROTEIN  
 i i US-08-208-007A-12

Query Match 64 KPIFYPLSNYRDVQFGEIGTPONFTVAFDTGSNHWPSRCHFVPCWLMHHRD 123  
 Db 59 NPSFVPLSKMNTQFGTIGTPONFTVAFDTGSNHWPSRCHFVPCWLMHHRN 118

Query Match 64 PKASSSFQANGTKFAQYGTGRDVQFGEIGTPONFTVAFDTGSNHWPSRCHFVPCWLMHHRD 183  
 Db 119 PKASSSFQANGTKFAQYGTGRDVQFGEIGTPONFTVAFDTGSNHWPSRCHFVPCWLMHHRF 178

Query Match 64 DGLLGLGFPLISVEVRPMDFVQGLLQKPVFSYLNRLDPEEDGGBNLGSDDPAHY 243  
 Db 179 DGLLGLGFPLISVEVRPMDFVQGLLQKPVFSYLNRLDPEEDGGBNLGSDDPAHY 238

Query Match 64 PPPAGPPMILGDVFLGTYVAVFDGMKSSARYGLARARTRGADLGMEATAQOF----P 419  
 Db 239 VPPITFPIPTIPAYQWINEVSQVTGSLCAQCSAIDDTGTSLSITGSEEYRALKA 298

Query Match 64 GGIPLLAGGYTILCSEIPKLPAVSGWENLTAHDYVICTRNGYRLCLSGLGSETAQOF----P 363  
 Db 304 PPPAGPFMILGDVFLGTYVAVFDGMISARVGLARARTRGADLGMEATAQOF----P 419

Query Match 64 GGPFLNGCYFIQCSKTPPLPPVAVFDGDKMVGPVGLARASRSSTDRAERRTQAFKKRP 418  
 Db 359 PKAGPMLWLGDVFLGTYVAVFDGDKMVGPVGLARASRSSTDRAERRTQAFKKRP 418

Query Match 64 QY 244 IPPLTFVPTVDPAYQTHMERYKVGPGLTLCAGCAAILDGTSLLITGPTBIRALHAI 303  
 Db 239 VPLTFPTVDPAYQWHEMSVKGTVSLAQGSAILDTGTSLLTGSPSETRALKA 298

Query Match 64 QY 304 GG1PLLAGGYTILCSEIPKLPAVSGWENLTAHDYVICTRNGYRLCLSGLGSETAQOF----P 363  
 Db 299 GGPFLNGCYFIQCSKTPPLPPVAVFDGDKMVGPVGLARASRSSTDRAERRTQAFKKRP 418

Query Match 64 QY 364 PPPAGPPMILGDVFLGTYVAVFDGMKSSARYGLARARTRGADLGMEATAQOF----P 419  
 Db 420 G 420

Query Match 64 QY 420 G 419  
 Db 419 G 419

Qy 115 PCWLEHHRFDPKASSSFQANGTKFAI QYGTGRVDGILSEDKLTI-----GGIKGA 163  
 Db 116 ACWIHKYNSDKSSYVKGNTSDFDHYGSGLLISQTYSVQASASSASAAGGVKTB 175  
 Qy 164 SVIFGEALWEISLYVPAFAHEDGILGEPFILSVEGVRPMDFVLYVEQGLLIDKPVSFYLN 223  
 Db 176 RQVGEATKQDGITFLAAKEDGILGMAYPRISVNVNLVPEVDNLNMQKLTDQNISSYLSR 235  
 Qy 224 DPEEPDGELMVGSDPAHYTPLLTVFVPTVTPAYNOIHMERRVKVKGPGLLCAKGAAILD 283  
 Db 236 DPDAQPGELMLGGTTSKYRGSLSYLNTRKAYQVHDLOVEASGLTCKEGEATYD 295  
 Qy 284 TGTSLITGPTEEIRAHAAIGGIPILLAGEYLILCSEIPKLPAVSPFLGGWENLTADHDY 343  
 Db 296 TGTSLMVGVDDEVRELOKAIGGIPILLAGEYLILCSEIPKLPAVSPFLGGWENLTADHDY 355  
 Qy 344 IOTTRANGVRCLSLSGFQALDYPAPPAGFWIILGDFVPLGTYTAWFDRGDMKSSARVGLARA 401  
 Db 356 LKVSAQAKTLCLSGMGMDDPPSGLWLWLGDFVFIGRYTVFDR---DNNRVGEAE 409

RESULT<sup>13</sup>  
 US-08-974-691-4  
 ; Sequence 4, Application US/08974691  
 ; Patent No. 6225103  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Keolisch, Gerald  
 ; APPLICANT: Lin, Xinli  
 ; APPLICANT: Tang, Jordan  
 ; TITLE OF INVENTION: Cloning and Characterization of Napsin  
 ; NUMBER OF SEQUENCES: 14  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Patrea L. Pabst  
 ; STREET: 2800 One Atlantic Center, 1201 W. Peachtree  
 ; CITY: Atlanta  
 ; STATE: GA  
 ; COUNTRY: USA  
 ; ZIP: 30309-4500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: FLOPPY DISK  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US 08/974, 691  
 FILING DATE: 20-NOV-1997  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 60/031, 196  
 FILING DATE: 20-NOV-1996  
 PRIORITY DATA:  
 APPLICATION NUMBER: US 60/046, 126  
 FILING DATE: 09-MAY-1997  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Patrea L.  
 REGISTRATION NUMBER: OMRF 166  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 404-873-8794  
 TELEFAX: 404-873-8795  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 412 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 ORIGINAL SOURCE:  
 ORGANISM: Homo sapiens  
 US-08-974-691-4

Query Match 45.4%; Score 1015; DB 4; Length 412;  
 Best Local Similarity 46.9%; Pred. No. 3.5e-96;  
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

Qy 1 MSPPPLQPLLPLUNVEPSGATLIRPLHRYQPGRTINLRLGWR-----PAELP 54  
 Db 1 MQSSSLPLACLL---AAPASA-LVRLHKEITSIRTMSEVGSVEDLIAGPVSKY 55  
 Qy 55 KLGASPSPGDKPIFVPLSNTRDQVYFGETGLGTPQNPFYAFDTGSNLWVPSRCHFFSV 114  
 Db 56 SQAVPATVTEGPIPVYLNMDAQYGEIGITGPQCFVFDIGSNLWVPSRCHFFSV 115  
 Qy 115 PCWLHHRFDPKASSSFQANGTKFAI QYGTGRVDGILSEDKLTI-----GGIKGA 163  
 Db 116 ACWIHKYNSDKSSYVKGSLSYLNTRKAYQVHDLOVEASGLTCKEGEATYD 295  
 Qy 116 RQVGEATKQDGITFLAAKEDGILGMAYPRISVNVNLVPEVDNLNMQKLTDQNISSYLSR 235  
 Qy 224 DPEEPDGELMVGSDPAHYTPLLTVFVPTVTPAYNOIHMERRVKVKGPGLLCAKGAAILD 283  
 Db 236 DPDAQPGELMLGGTTSKYRGSLSYLNTRKAYQVHDLOVEASGLTCKEGEATYD 295  
 Qy 284 TGTSIITGPPEIRALHAIAIGGIPILLAGEYLILCSEIPKLPAVSPFLGGWENLTADHDY 343  
 Db 296 TGTSIIMVGPDVERELQRAIGAVPQIQQGYMIPCEKVSTLPALTIKLGKGYKLSPEDYT 355  
 Qy 344 IOTTRANGVRCLSLSGFQALDYPAPPAGFWIILGDFVPLGTYTAWFDRGDMKSSARVGLARA 401  
 Db 356 LKVSAQAKTLCLSGMGMDDPPSGLWLWLGDFVFIGRYTVFDR---DNNRVGEAE 409

RESULT<sup>14</sup>  
 US-08-915-095A-12  
 ; Sequence 12, Application US/08915095A.  
 ; Patent No. 6383153  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hastings, et al.  
 ; TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATHEPSIN  
 ; FILE REFERENCE: PF107D4  
 ; CURRENT APPLICATION NUMBER: US/08/915, 095A  
 ; CURRENT FILING DATE: 1997-08-20  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 12  
 ; LENGTH: 412  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-08-915-095A-12

Query Match 45.4%; Score 1015; DB 4; Length 412;  
 Best Local Similarity 46.9%; Pred. No. 3.5e-96;  
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

Qy 1 MSPPPLQPLLPLUNVEPSGATLIRPLHRYQPGRTINLRLGWR-----PAELP 54  
 Db 1 MQSSSLPLACLL---AAPASA-LVRLHKEITSIRTMSEVGSVEDLIAGPVSKY 55  
 Qy 55 KLGASPSPGDKPIFVPLSNTRDQVYFGETGLGTPQNPFYAFDTGSNLWVPSRCHFFSV 114  
 Db 56 SQAVPATVTEGPIPVYLNMDAQYGEIGITGPQCFVFDIGSNLWVPSRCHFFSV 115  
 Qy 115 PCWLHHRFDPKASSSFQANGTKFAI QYGTGRVDGILSEDKLTI-----GGIKGA 163  
 Db 116 ACWIHKYNSDKSSYVKGSLSYLNTRKAYQVHDLOVEASGLTCKEGEATYD 295  
 Qy 116 RQVGEATKQDGITFLAAKEDGILGMAYPRISVNVNLVPEVDNLNMQKLTDQNISSYLSR 235  
 Qy 224 DPEEPDGELMVGSDPAHYTPLLTVFVPTVTPAYNOIHMERRVKVKGPGLLCAKGAAILD 283  
 Db 236 DPDAQPGELMLGGTTSKYRGSLSYLNTRKAYQVHDLOVEASGLTCKEGEATYD 295

Query Match 45.4%; Score 1015; DB 3; Length 412;

Db

Qy 284 TGTSLLITGPTEEIRALHAIAIGGIPIIAGLEYTILCSEIPKLPAVSFLGGYWENLTAHDYV 343  
 Db 296 TGTSLMVGPTDEVRLQKAAGAVPLIQGEMIPCKVSTPAITKLGGKYKUSPEDDT 355

Qy 344 IQTTRNGVRCLSGFOALDYPAPPAGFPMWILGDVFELGYTAYVEDRCDMKSSARVGLARA 401  
 Db 356 LKVSDAGKTLCLSGFMGMDDIPPPSGPLWILGDVFGRYTVDRLGDR---DNNRVFAEA 409

RESULT 15

US -08-798-096-12  
 ; Sequence 12, Application US/08798096  
 ; Patent No. 6387682  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Hastings, et al.  
 ; TITLE OF INVENTION: HUMAN OSTEOCLAST-DERIVED CATEPSIN  
 ; FILE REFERENCE: PFI07D2  
 ; CURRENT APPLICATION NUMBER: US/08/798, 096  
 ; CURRENT FILING DATE: 1997-02-12  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SEQ ID NO 12  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; LENGTH: 412  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US -08-798-096-12

Query Match 45.4%; Score 1015; DB 4; Length 412;  
 Best Local Similarity 46.9%; Pred. No. 3.5e-96;  
 Matches 196; Conservative 71; Mismatches 125; Indels 26; Gaps 5;

Qy 1 MSPPPLQPLLLLPLNVEPSEGATLIRIPLHRYOPGRATLNLRGWRE-----PAELP 54  
 Db 1 MQPSSILPLAICLL---APASA-LVRPLHFKTSITRMSEVGSVDELIAKGPVSKY 55

Qy 55 KLGASPDKPIFIYPLSNYDVOYFGEIGLGTTPONFTYAFDTGSNNLYWPSRICHHFFSY 114  
 Db 56 SQAIVAVTEGPIPEVKNNDAAQYGEIGLGTTPPOCFVTFDTGSNLWVPSIHKLLDI 115

Qy 115 PCWLHHRDPKASSSFQANGTKFAIQYGRDVGDGLISEDKLTI-----GGIKGA 163  
 Db 116 ACWTHHKYNSDKSSTYVKNGTSFDTHYGSSSLGTSQNTVSVPQCASSASALGGVKB 175

Qy 164 SVIFGEALWEPSLVAFAHDDGILGIGFPLUSVEGVPMDFVLVEQGLDJDKPVESFYLR 223  
 Db 175 RQVFEATRQGIFTAAKEDGILGMAPIRISVNVLPLFDNMQQLWDQNIISFYLSR 235

Qy 224 DPEEEDPGGELVPLGGSDPAHYTIPPLFVPTVPAWQIHMERVKVGPGLTCAKGCAATLD 283  
 Db 236 DPDRQPGGEMLGGTDSKYKGSLSYLNVTRKAWQVHJLQVEASGLTICKEGEATD 295

Qy 284 TGTSLLITGPTEEIRALHAIAIGGIPIIAGLEYTILCSEIPKLPAVSFLGGYWENLTAHDYV 343  
 Db 296 TGTSLMVGPTDEVRLQKAAGAVPLIQGEMIPCKVSTPAITKLGGKYKUSPEDDT 355

Qy 344 IQTTRNGVRCLSGFOALDYPAPPAGFPMWILGDVFGRYTVDRLGDR---DNNRVFAEA 401  
 Db 356 LKVSDAGKTLCLSGFMGMDDIPPPSGPLWILGDVFGRYTVDRLGDR---DNNRVFAEA 409

Search completed: June 2, 2004, 20:23:16  
 Job time : 30.2707 secs

ALIGNMENTS						
RESULTS						
st-processing:	Minimum Match 0%					
	Maximum Match 100%					
	Listing First 45 summaries					
atabase :	A_Geneseq_29Jan04:*					
	1: geneseqP1980s:*					
	2: geneseqP1990s:*					
	3: geneseqP2000s:*					
	4: geneseqP2010s:*					
	5: geneseqP2002s:*					
	6: geneseqP2003as:*					
	7: geneseqP2003bs:*					
	8: geneseqP2004s:*					
tal number of hits satisfying chosen parameters:	1586107					
minimum DB seq length:	0					
maximum DB seq length:	2000000000					
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.						
SUMMARIES	%	Query	Match	Length	DB	ID
ult	No.	Score	Match	Length	DB	ID
1	2238	100.0	420	2	AAV06435	
2	2238	100.0	420	3	AAV44809	
3	2238	100.0	420	3	AAV44457	
4	2232	99.7	420	2	AAW54878	
5	2232	99.7	420	6	AAE37358	
6	2232	99.7	433	5	AQO20497	
7	2069.5	92.5	395	2	AAW37958	
8	1897	84.8	438	2	AAW57042	
9	1897	84.8	451	2	AAW54877	
10	1887	84.3	433	3	AAV44810	
11	1792.5	76.1	390	4	AAU09094	
12	1678.9	57.0	449	2	AAW57043	
13	1561.5	69.7	419	3	AAV79177	
14	1343	60.0	288	4	AAU23066	
15	1328	59.3	262	4	AAW8539	
16	1328	59.3	262	5	ABG76585	
17	1328	59.3	262	5	ABG54720	
18	1179	52.7	285	3	ABG5332	
19	1050	46.9	212	4	ABG85560	
20	1050	46.9	212	5	ABG76606	
21	1050	46.9	212	5	ABG54722	
22	1037	46.3	410	4	AAU01672	
23	1037	46.3	410	5	ABG53963	
24	1037	46.3	410	6	ADG5722	
25	1037	46.3	410	6	ADG40983	







Db	Accession	Protein Name	Sequence	Source	Similarity	Pred. No.	Matche	Details	Gaps
Db	181	AHFDGILGGI GFP ILL VEGTRPPMVLV FSSYLNDPEE PGGLV LGSDP	240	Best Local	99.8%	2.7e-202;	0;	Mismatches	0;
Dy	241	AHYIPLPTVPTVTPAYNQIHMERYVKVGPGLCAKGCPAII DGTSLITGPTEEIRALH	300	Conservative	0;	0;	4:19;	Indels	0;
Dy	241	AHYIPLPTVPTVTPAYNQIHMERYVKVGPGLCAKGCPAII DGTSLITGPTEEIRALH	300	Qy	1	MSPPDQLQPLL LLLNVEPSGATLIRIPLHRVQGRPRPNNLIGWRREP AELPLIGAPS	60		
Db	241	AHYIPLPTVPTVTPAYNQIHMERYVKVGPGLCAKGCPAII DGTSLITGPTEEIRALH	300	Db	14	MSPPDQLQPLL LLLNVEPSGATLIRIPLHRVQGRPRPNNLIGWRREP AELPLIGAPS	73		
Dy	301	AAIGGIPPLAGEYIILCSEIPKLPAVSTLFGWFLNLTADYV IOTTRNGVRLLSGFA	360	Qy	61	PGDKPDI FVPLSNTYDQYF BIGLTPONFTVAFDTGSSNLWVPSRRCFFVPCWLHH	120		
Db	301	AAIGGIPPLAGEYIILCSEIPKLPAVSTLFGWFLNLTADYV IOTTRNGVRLLSGFA	360	Db	74	PGDKPDI FVPLSNTYDQYF BIGLTPONFTVAFDTGSSNLWVPSRRCFFVPCWLHH	133		
Dy	361	LDVPPAGFPFWI LDGVFLGTYVAYFDRGMKSSARVGLAR ARTRGADLG WGETAQAFQFG	420	Qy	121	RDPKASSF QANGT KFA IQYGTGAS YFGEALWEP SLVFAF	180		
Db	361	LDVPPAGFPFWI LDGVFLGTYVAYFDRGMKSSARVGLAR ARTRGADLG WGETAQAFQFG	420	Db	134	RDPKASSF QANGT KFA IQYGTGAS YFGEALWEP SLVFAF	193		
Dy	AAO20497	standard; protein; 433 AA.	AAO20497	Qy	181	AHF DGLGQGPFISVEGVRPPMDLV EQLDKEVFSFLINRDEEPDGELVUGGSDP	240		
Dy	AAO20497;		AAO20497;	Db	194	AHF DGLGQGPFISVEGVRPPMDLV EQLDKEVFSFLINRDEEPDGELVUGGSDP	253		
Dy	27-JUN-2002 (first entry)		27-JUN-2002 (first entry)	Qy	241	AHY1BPLTFVPTVTPAYNQIHMERYVKVGPGLCAAILDTGTEIRALH	300		
Dy				Db	254	AHY1BPLTFVPTVTPAYNQIHMERYVKVGPGLCAAILDTGTEIRALH	313		
Dy		Protein of NAP1 from aspartyl protease-related family.		Qy	301	AAIGGIPPLAGEYIILCSEIPKLPAVSTLFGWFLNLTADYV IOTTRNGVRLLSGFA	360		
Dy		Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta; amyloid precursor protein; tissue specific expression control; human APP; APP pathway modulator; gene therapy.		Db	314	AAIGGIPPLAGEYIILCSEIPKLPAVSTLFGWFLNLTADYV IOTTRNGVRLLSGFA	373		
Dy		Homo sapiens.		Qy	361	LDVPPAGFPFWI LDGVFLGTYVAYFDRGMKSSARVGLAR TRGDLG WGETAQAFQFG	420		
Dy		WO200226820-A2.	WO200226820-A2.	Db	374	LDVPPAGFPFWI LDGVFLGTYVAYFDRGMKSSARVGLAR TRGDLG WGETAQAFQFG	433		
				RESULT 7					
				AAW37958					
				ID	AAW37958	Standard; protein; 395 AA.			
				XX	AAW37958;				
				AC	AAW37958;				
				XX	AAW37958;				
				DT	21-AUG-1998	(first entry)			
				XX					
				DE	Amino acid sequence of human cathepsin polypeptide-2.				
				XX	Human cathepsin polypeptide-2; HCP-2; metastasis; antibody; agonist; antagonist; tumour; arthritis; Alzheimer's disease; HCP-1; Huntington's disease; mucolipidosis.				
				XX	Homo sapiens.				
				OS					
				XX					
				PN	W0913484-A1.				
				XX					
				PD	02-APR-1998.				
				XX					
				PF	25-SEP-1997;	97WO-US017175.			
				XX					
				PR	26-SEP-1996;	96US-00723938.			
				XX					
				PA	(INCY-) INCYTE PHARM INC.				
				XX					
				PI	Bandman O, Coleman R;				
				XX					
				DR	WPI: 1998-230698/20.				
				XX	N-PPDB; AAV31665.				
				PT	Human cathepsins and related nucleic acids, vectors and products - useful for treatment and diagnosis of e.g. tumours, metastases, inflammation, neurological disease etc.				
				XX	Claim 15; Fig 5A-5D; 69pp; English.				
				PS	This is the amino acid sequence of the human cathepsin polypeptide-2 (HCP -2), which is involved in inflammation, metastasis and peptide/proenzyme processing. HCP related products (e.g. antibodies, agonists, and antagonists) are potentially useful for treating tumours, metastases, inflammation, arthritis, and peptidase inhibitors.				
				CC	CC	CC	CC	CC	CC
				SQ	Sequence 433 AA;	Score 2232;	DR 5;	Length 433;	Query Match

CC Alzheimer's and Huntington's disease, and mucolipidosis. Fragments of  
 CC HCP-2 are useful diagnostically (to detect or quantify gene expression),  
 CC to monitor the effects of treatment and to map the corresponding genomic  
 XX sequences

SQ Sequence 395 AA;

Query Match 92.5%; Score 2069.5; DB 2; Length 395;  
 Best Local Similarity 93.8%; Pred. No. 5.6e-187;  
 Matches 394; Conservative 0; Mismatches 1; Indels 25; Gaps 1;

Db 1 MSPPPLQLPILLPLINVEPSGATLIRIPLHRVQGRTRNLIRGWRPEAELPKLGAPS 60

Db 1 MSPPPLQLPILLPLINVEPSGATLIRIPLHRVQGRTRNLIRGWRPEAELPKLGAPS 60

Qy 61 PGDKP1FVPLSNYRDYQFGETGLGPQQNFTVAPDTGSNLWVPBRCHFFSVPWLHH 120

Db 61 PGDKP1FVPLSNYRDYQFGETGLGPQQNFTVAPDTGSNLWVPBRCHFFSVPWLHH 120

Qy 121 RFDPKASSFOQANGTKPAIQTGTRVGDGLSEDKLTTIGKIASVIFGEALWEPSLVEAF 180

Db 121 RFDPKASSFOQANGTKPAIQTGTRVGDGLSEDKLTTIGKIASVIFGEALWEPSLVEAF 180

Qy 181 AHFDGILGLGFPTLSVEGVRPFMDVILVEQGLIDKPVSFYLNRPDPEBPGGBLVTLGGSDP 240

Db 181 AHFDGILGLGFPTLSVEGVRPFMDVILVEQGLIDKPVSFYLNRPDPEBPGGBLVTLGGSDP 240

Db 181 AHFDGILGLGFPTLSVEGVRPFMDVILVEQGLIDKPVSFYLNRPDPEBPGGBLVTLGGSDP 240

Qy 241 AHYIPPLTFVPTVTPAYWQIMERVKVGPGTLCAKGCAAIDTGTSLITGPEEIRALH 300

Db 241 AHYIPPLTFVPTVTPAYWQIMERVKVGPGTLCAKGCAAIDTGTSLITGPEEIRALH 300

Qy 301 AAIIGGIPLLAGEYIILCSEIPLKPAYSFILLGGWVNLTAHDVY1QTRNGVRCLSGFQA 360

Db 301 AAIIGGIPLLAGEYIILCSEIPLKPAYSFILLGGWVNLTAHDVY1QTRNGVRCLSGFQA 360

Qy 361 LDVPPPAGPFWLIGDVFGLTYVAVFDRGDKMSSARYGLARARTGRADLGWGETAOQFPG 420

Db 350 -----DVFGLTYVAVFDRGDKMSSARYGLARARTGRADLGWGETAOQFPG 395

Claim 14; Page 20; 32pp; English.

The present sequence represents a human aspartic protease. The present

invention describes novel human aspartic proteases and also EGFRs from

human cDNA libraries having partial DNA sequences which encodes an

aspartic protease. Compounds which inhibit aspartic protease, especially

antibodies can be used in therapy where needed. The protease can also be

used in therapy where needed. Important functions of aspartic proteases

are the processing of endothein and pro-opiomelanocortin prohormones.

They may also be involved in the processing of serum amyloid A protein.

Sequence 438 AA;

Query Match 84.8%; Score 1897; DB 2; Length 438;

Best Local Similarity 86.0%; Pred. No. 1.4e-170;

Matches 361; Conservative 16; Mismatches 43; Indels 0; Gaps 0;

Qy 1 MSPPPLQLPILLPLINVEPSGATLIRIPLHRVQGRTRNLIRGWRPEAELPKLGAPS 60

Db 1 MSPPPLQLPILLPLINVEPSGATLIRIPLHRVQGRTRNLIRGWRPEAELPKLGAPS 60

Qy 61 PGDKP1FVPLSNYRDYQFGETGLGPSSVPPONETVAPDTGSNLWVPSSRCHFFSVPWLHH 120

Db 61 PGDKP1FVPLSNYRDYQFGETGLGPSSVPPONETVAPDTGSNLWVPSSRCHFFSVPWLHH 120

Db 61 PGDKP1FVPLSNYRDYQFGETGLGPSSVPPONETVAPDTGSNLWVPSSRCHFFSVPWLHH 120

Qy 121 RFDPKASSFOQANGTKPAIQTGTRVGDGLSEDKLTTIGKIASVIFGEALWEPSLVEAF 180

Db 121 RFDPKASSFOQANGTKPAIQTGTRVGDGLSEDKLTTIGKIASVIFGEALWEPSLVEAF 180

Qy 181 AHYIPPLTFVPTVTPAYWQIMERVKVGPGTLCAKGCAAIDTGTSLITGPEEIRALH 300

Db 181 AHYIPPLTFVPTVTPAYWQIMERVKVGPGTLCAKGCAAIDTGTSLITGPEEIRALH 300

Qy 241 AHYIPPLTFVPTVTPAYWQIMERVKVGPGTLCAKGCAAIDTGTSLITGPEEIRALH 300

Db 241 AHYIPPLTFVPTVTPAYWQIMERVKVGPGTLCAKGCAAIDTGTSLITGPEEIRALH 300

Qy 301 AAIGGIPLLAGEYIILCSEIPLKPAYSFILLGGWVNLTAHDVY1QTRNGVRCLSGFQA 360

Db 301 AAIGGIPLLAGEYIILCSEIPLKPAYSFILLGGWVNLTAHDVY1QTRNGVRCLSGFQA 360

Qy 361 LDVPPPAGPFWLIGDVFGLTYVAVFDRGDKMSSARYGLARARTGRADLGWGETAOQFPG 420

Db 361 LDVPPPAGPFWLIGDVFGLTYVAVFDRGDKMSSARYGLARARTGRADLGWGETAOQFPG 420

RESULT 9

AAW54877

ID AAW54877 standard; protein; 438 AA.

XX

AC AAW54877;

XX

DE 26-OCT-1998 (first entry)

XX

DE Human napsin A protein.

XX

KW Napsin A; splicing; clone; screening; human liver cDNA library;

XX

KW aspartic protease; ss.

OS Homo sapiens.

XX

FH Key

FT Misc-difference 433

FT Misc-difference 434

FT Misc-difference 435

FT Misc-difference 436

FT Misc-difference 437

FT Misc-difference 438

FT Misc-difference 439

FT Misc-difference 440

FT Misc-difference 441

FT Misc-difference 442

FT Misc-difference 443

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FT Misc-difference 626

FT Misc-difference 627

FT Misc-difference 628

FT Misc-difference 629

FT Misc-difference 630

FT Misc-difference 631

FT Misc-difference 632

FT Misc-difference 633

FT Misc-difference 634





panic disorder, learning disabilities, amyotrophic lateral sclerosis, psychoses, autism, sleep disorders), immune system disorders (e.g. Hashimoto's thyroiditis), renal and musculo-skeletal system disorders, central nervous system disorders (e.g. multiple sclerosis, ischaemic brain injury and/or stroke), infectious diseases, diabetes mellitus, immunological disorders (e.g. asthma, acquired immunodeficient syndrome (AIDS), leukaemia, rheumatoid arthritis, inflammatory bowel disease, sepsis, acne, psoriasis and lupus erythematosus), neural system disorders, respiratory disorders, olfactory disorders and wound healing.

The present sequence represents an NEP of the invention

Sequence 390 AA;

Query	76.1%; Score 1702.5; DB 4; Length 390;	FT Misc-difference 440 /note= "encoded by GNC"
Best Local Similarity	93.3%; Prod. No. 3e-152;	FT Misc-difference 440 /note= "encoded by TGA"
Matches	334; Conservative 7; Mismatches 15; Indels 45; Gaps 4;	FT Misc-difference 442 /note= "encoded by NGA"
Qy	21 PSGATLIRPLHRVQPGRRITLNLRGWRPAELPKLGAPSQPGDKP1KFVPLSNYRDVQYFG 80	FT Misc-difference 442 /note= "encoded by NGA"
Db	34 PSGATLIRPLHRVQGRRLNLRGWRPAELPKLGAPSQPGDKP1KFVPLSNYKG---- 88	XX WO811236-A1.
Qy	81 EIGLTGPNONFTVAFDTGSSNLWYPSRQHFFSVPWCMILHHRDPKASSFQANGTKFQI 140	XX PD 19-MAR-1998.
Db	89 -----WHRFRDPKASTP-SSQMDQFAIQ 111	XX PF 09-SEP-1997;
Qy	141 YGTGRVDGILSEDKLITGGIKGASVIFGE-AIWFPSLVEFAHPDGFLGLGFPLSVEG 199	XX PR 11-SEP-1996;
Db	112 YGTGRVHGILSEDKLITGGIKGASVIFGE-QPGL--RFCPDGFLGLGFPLSVEG 169	XX PR 09-TWO-GB002426.
Qy	200 RPPMDVLVYEGQLIDKPVFESFYLNRDPEEDPGGELVLGSQSDPAHYTIPPLTFVPPVTPAYWQ 259	XX PA (SMIK ) SMITHKLINE BEECHAM PLC.
Db	170 RPPMDVLVYEGQLIDKPVFESFYLNRDPEEDPGGELVLGSQSDPAHYTIPPLTFVPPVTPAYWQ 229	XX PA (UYWA-) UNITV WALES.
Qy	260 THMERVKVYQGLTLCAKGAAILDGTGTSITGPEETIRALHAAGGIPLAGYIILCSE 319	XX PI Powell D, Kay J, Hill J;
Db	230 THMERVKVYQGLTLCAKGAAILDGTGTSITGPEETIRALHAAGGIPLAGYIILCSE 289	XX XX WPI; 1998-207396/18.
Qy	320 IPKLPAVSFLGGWENLTAHDYVQTTRNGVRCLSGQALDVPFPFWLGDVFLG 379	DR N-PSDB; AAV28624.
Db	299 IPKLPAVSFLGGWENLTAHDYVQTTRNGVRCLSGQALDVPFPFWLGDVFLG 349	XX Human aspartic protease and related DNA - which may be involved in processing of endothelin and pro-opiomelanocortin pro-hormone(s).
Qy	380 TYAVFDRGDMKSSARVGLRARTRGADLGWGETAQAOFPG 420	XX PT Human aspartic protease and related DNA - which may be involved in processing of endothelin and pro-opiomelanocortin pro-hormone(s).
Db	350 TYAVFDRGEMKSSARVGLRARTRGADLGWGETAQAOFPG 390	XX XX Claim 14; Page 23; 32pp; English.

Query Match	75.0%; Score 1678.5; DB 2; Length 449;	XX XX The present sequence represents a human aspartic protease. The present invention describes novel human aspartic proteases and also ESTs from human cDNA libraries having partial DNA sequences which encodes an aspartic protease. Compounds which inhibit aspartic protease, especially antibodies can be used in therapy where needed. The protease can also be used in the processing of endothelin and pro-opiomelanocortin pro-hormones. They may also be involved in the processing of serum amyloid A protein.
Best Local Similarity	81.1%; Prod. No. 6.e-150;	CC CC
Matches	327; Conservative 18; Mismatches 55; Indels 3; Gaps 3;	CC CC
Qy	9 PILLPLPLNVEPAGATLIRPLRQVQGRRTNLRLGRWREPAPLKPGAPSQPGDKP1FV 68	CC CC
Db	28 PSLLPLPLNVEPAGATLIRPLRQVHGRRTNLRLGWKGPKAPLKPGAPSQPGDKPASV 87	CC CC
Qy	69 PLSNYRDVOYFGEIGLGPQNFTVAFDTGSSNLWVPSRRCHFSPCPWMLHHRDPKASS 128	CC CC
Db	88 PLSKELDAQFEGIGLGPQNFTVAFDTGSSNLWVPSRRCHFSPCPWMLHHRFPNPNASS 147	CC CC
Qy	129 SFQANGTKPAAIQYGTGRDGLSSEDKLITGGIKGASVIFGEAWEPSLVFAFAHFDGILG 188	CC CC
Db	148 SEKPSGTTKPAIQYGTGRDGLSSEDKLITGGIKGASVIFGEAWEPSLVFAFAHFDGILG 207	CC CC
Qy	189 LGFPPLISVEGVRPPMDVLVEQGLIDKPVPSFLNRDPERPDGELVLGSQSDPAHYTIPPL 248	CC CC
Db	208 LGFPPLISVEGVRPPMDVLVEQGLIDKPVPSFYNRDPEPYVNG3ELVLGSSDPAHYTIPPLN 267	CC CC
Qy	249 FVPVTVPAWQIHMVKYQGLTCAKGAAILDGTGTSITGPEETIRALHAAGGIPLAGYIILCSE 307	CC CC
Db	268 FVPVTVPAWQIHMVKYQGLTCAKGAAILDGTGTSITGPEETIRALHAAGGIPLAGYIILCSE 327	CC CC
Qy	308 LLAGEYXILCSEIPLCPAYSFLLGQGMWENLTAHDYVQTTRNG-VRLCLSGFOADVPPP 366	CC CC
Db	328 LLAGEYXILCSEIPLCPAYSLLGQGMWENLTAHDYVQTTRNG-VRLCLSGFRADIIARA 387	CC CC
Qy	367 AGPFWLGDVFLGTVAVEDRGDMKSSARVGLRARTRGADLG 409	CC CC
Db	388 EGFWNLGEFWWG-1CDRFRTGTXEANPSXLACTVALGPXSG 429	CC CC

RESULT 1.2  
AAN57043 standard; protein; 449 AA.  
AC AAW57043;  
XX DT 29-JUL-1998 (first entry)  
XX DE Human aspartic protease encoding cDNA SEQ ID NO:15.  
XX KW Human; aspartic protease; EST; endothelin; serum amyloid A protein; pro-opiomelanocortin prohormone.  
XX OS Homo sapiens.  
XX FH Key-Misc-difference 1 Location/Qualifiers  
FT Misc-difference 1 /note= "encoded by NAA"  
FT Misc-difference 1 /note= "encoded by TGA"  
FT Misc-difference 1 /note= "encoded by ANA"  
FT Misc-difference 410 /note= "encoded by TGA"  
FT Misc-difference 417 /note= "encoded by TGA"  
FT Misc-difference 427 /note= "encoded by TGN"  
FT Misc-difference 433 /note= "encoded by TGN"  
RESULT 1.3  
AAV79177



PR 22-AUG-2000; 2000US-0226681P.  
 PR 22-AUG-2000; 2000US-022688P.  
 PR 22-AUG-2000; 2000US-0227182P.  
 PR 23-AUG-2000; 2000US-0227009P.  
 PR 30-AUG-2000; 2000US-0228924P.  
 PR 01-SEP-2000; 2000US-0229287P.  
 PR 01-SEP-2000; 2000US-0229343P.  
 PR 01-SEP-2000; 2000US-0229344P.  
 PR 01-SEP-2000; 2000US-0229345P.  
 PR 05-SEP-2000; 2000US-0229509P.  
 PR 05-SEP-2000; 2000US-0229513P.  
 PR 06-SEP-2000; 2000US-0230437P.  
 PR 06-SEP-2000; 2000US-0230438P.  
 PR 08-SEP-2000; 2000US-0231242P.  
 PR 08-SEP-2000; 2000US-0231243P.  
 PR 08-SEP-2000; 2000US-0231244P.  
 PR 08-SEP-2000; 2000US-0231413P.  
 PR 08-SEP-2000; 2000US-0231414P.  
 PR 08-SEP-2000; 2000US-0232080P.  
 PR 08-SEP-2000; 2000US-0232081P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 PR 14-SEP-2000; 2000US-0232397P.  
 PR 14-SEP-2000; 2000US-0231419P.  
 PR 14-SEP-2000; 2000US-0231419P.  
 PR 14-SEP-2000; 2000US-0232400P.  
 PR 14-SEP-2000; 2000US-0232401P.  
 PR 14-SEP-2000; 2000US-0233063P.  
 PR 14-SEP-2000; 2000US-0233064P.  
 PR 14-SEP-2000; 2000US-0233065P.  
 PR 21-SEP-2000; 2000US-0234233P.  
 PR 25-SEP-2000; 2000US-0234274P.  
 PR 25-SEP-2000; 2000US-0234997P.  
 PR 25-SEP-2000; 2000US-0234998P.  
 PR 27-SEP-2000; 2000US-0235484P.  
 PR 27-SEP-2000; 2000US-023586P.  
 PR 29-SEP-2000; 2000US-0236327P.  
 PR 29-SEP-2000; 2000US-02363367P.  
 PR 29-SEP-2000; 2000US-0236338P.  
 PR 29-SEP-2000; 2000US-0236369P.  
 PR 29-SEP-2000; 2000US-0238344P.  
 PR 02-OCT-2000; 2000US-0238834P.  
 PR 02-OCT-2000; 2000US-0238842P.  
 PR 02-OCT-2000; 2000US-0237037P.  
 PR 02-OCT-2000; 2000US-0237038P.  
 PR 02-OCT-2000; 2000US-0237040P.  
 PR 13-OCT-2000; 2000US-023935P.  
 PR 13-OCT-2000; 2000US-0239937P.  
 PR 20-OCT-2000; 2000US-0240960P.  
 PR 20-OCT-2000; 2000US-0241221P.  
 PR 20-OCT-2000; 2000US-0241785P.  
 PR 20-OCT-2000; 2000US-0241786P.  
 PR 20-OCT-2000; 2000US-0241787P.  
 PR 20-OCT-2000; 2000US-0241808P.  
 PR 20-OCT-2000; 2000US-0241899P.  
 PR 20-OCT-2000; 2000US-0241826P.  
 PR 01-NOV-2000; 2000US-0244617P.  
 PR 08-NOV-2000; 2000US-0244614P.  
 PR 08-NOV-2000; 2000US-024675P.  
 PR 08-NOV-2000; 2000US-0246476P.  
 PR 08-NOV-2000; 2000US-0246477P.  
 PR 08-NOV-2000; 2000US-0246478P.  
 PR 08-NOV-2000; 2000US-024523P.  
 PR 08-NOV-2000; 2000US-024524P.  
 PR 08-NOV-2000; 2000US-024525P.  
 PR 08-NOV-2000; 2000US-024526P.  
 PR 08-NOV-2000; 2000US-024527P.  
 PR 08-NOV-2000; 2000US-024532P.  
 PR 08-NOV-2000; 2000US-024533P.  
 PR 08-NOV-2000; 2000US-0246609P.  
 PR 08-NOV-2000; 2000US-0246610P.  
 PR 08-NOV-2000; 2000US-0246611P.  
 PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.  
 PR 17-NOV-2000; 2000US-0249208P.  
 PR 17-NOV-2000; 2000US-0249209P.  
 PR 17-NOV-2000; 2000US-0249210P.  
 PR 17-NOV-2000; 2000US-0249211P.  
 PR 17-NOV-2000; 2000US-0249212P.  
 PR 17-NOV-2000; 2000US-0249213P.  
 PR 17-NOV-2000; 2000US-0249214P.  
 PR 17-NOV-2000; 2000US-0249215P.  
 PR 17-NOV-2000; 2000US-0249216P.  
 PR 17-NOV-2000; 2000US-0249217P.  
 PR 17-NOV-2000; 2000US-0249218P.  
 PR 17-NOV-2000; 2000US-0249244P.  
 PR 17-NOV-2000; 2000US-0249245P.  
 PR 17-NOV-2000; 2000US-0249264P.  
 PR 17-NOV-2000; 2000US-0249265P.  
 PR 17-NOV-2000; 2000US-0249297P.  
 PR 17-NOV-2000; 2000US-0249299P.  
 PR 17-NOV-2000; 2000US-0249300P.  
 PR 01-DEC-2000; 2000US-0250160P.  
 PR 01-DEC-2000; 2000US-0250391P.  
 PR 05-DEC-2000; 2000US-0251030P.  
 PR 05-DEC-2000; 2000US-0251988P.  
 PR 05-DEC-2000; 2000US-0251989P.  
 PR 06-DEC-2000; 2000US-0251479P.  
 PR 08-DEC-2000; 2000US-0251856P.  
 PR 08-DEC-2000; 2000US-0251868P.  
 PR 08-DEC-2000; 2000US-0251869P.  
 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0251990P.  
 PR 05-JAN-2001; 2000US-0254097P.  
 XX SEQ ID NO 10622: 1180PP; English.  
 (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Barash SC, Ruben SM;  
 XX DR WPI- 2001-465566/50.  
 XX DR N-SDDB; AAS40936.  
 XX Novel polypeptides and polynucleotides useful for diagnosing, preventing,  
 treating neural, immune system, muscular, reproductive, pulmonary,  
 cardiovascular, renal, proliferative disorders and cancerous diseases.  
 XX Claim 11; SEQ ID NO 10622: 1180PP; English.  
 PA XX  
 CC The present invention relates to the isolation of novel human enzyme  
 polypeptides, and the cDNA (AAS40935-AAS41684) and Genomic sequences  
 encoding them. The enzyme polypeptides of the invention may comprise the  
 functional classes of oxidoreductases, transferases, hydrolases, lyases,  
 isomerases or ligases. The sequences of the invention are useful in the  
 diagnosis, treatment, prevention and/or prognosis of a wide range of  
 disorders including hyperproliferative disorders (e.g. cancer),  
 autoimmune disorders (e.g. AIDS), autoimmune disorders (e.g.  
 arthritis), neurological disorders (e.g. Alzheimer's disease),  
 inflammatory disorders (e.g. phenylketonuria), cardiovascular disorders (e.g. asthma),  
 cardiovascular disorders (e.g. atherosclerosis), blood-related disorders  
 (e.g. haemophilia), reperfusion disorders (e.g. Influenza). The polynucleotides of the  
 invention can also be used in gene therapy. AAS40935-AAS41684 represent  
 the novel human enzyme polypeptides of the invention. Note: The sequence  
 data for this patent did not form part of the printed specification, but  
 was obtained in electronic format directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences  
 XX Sequence 288 AA;  
 SQ XX  
 Query Match 60.0%; Score 1343; DB 4; Length 288;  
 Best Local Similarity 99.6%; Pred. No. 2\_1e-118;  
 Matches 251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPPLQLLILPLNVEPSGATLIRPLHRVQPGRTINLRGWRPAELPKLGAPS 60

3 MSPPPLQPLLLLPLLNVEPSGATLIRIPLHRVQFRRILNLRGWREPAELPKLGAPS 62  
 Db CC treated include autoimmune diseases e.g. rheumatoid arthritis,  
 QY CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.  
 Db CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and  
 CC ocular disorders e.g. corneal infection. The polypeptides can also be  
 CC used to aid wound healing and epithelial cell proliferation, to prevent  
 CC skin aging due to sunburn, to maintain organs before transplantation and in  
 CC supporting cell culture of primary tissues to regenerate tissues and in  
 CC chemotaxis. The polypeptides can also be used as a food additive or  
 CC preservative to increase or decrease storage capabilities. The present  
 CC sequence represents a human secreted protein.  
 SQ Sequence 262 AA:

Query	Match	59.3%	Score 1328;	DB 4;	Length 262;
	Best Jocal Similarity	97.6%	Pred. No. 4.8e-117;		
	Mismatches	0;	Indels	0;	Gaps 0;

Qy 1 MSPPPLQPLLLLPLLNVEPSGATLIRIPLHRVQFRRILNLRGWREPAELPKLGAPS 60  
 Db 1 MSPPPLQPLLLLPLLNVEPSGATLIRIPLHRVQFRRILNLRGWREPAELPKLGAPS 60  
 Qy 61 PGDKP1FVPLSNYRDQYFGEIGLGPQNNTVAFTGSSNLWPSRCHFFSYCWLHH 120  
 Db 61 PGDKP1FVPLSNYRDQYFGEIGLGPQNNTVAFTGSSNLWPSRCHFFSYCWLHH 120  
 Qy 61 PGDKP1FVPLSNYRDQYFGEIGLGPQNNTVAFTGSSNLWPSRCHFFSYCWLHH 120  
 Db 61 PGDKP1FVPLSNYRDQYFGEIGLGPQNNTVAFTGSSNLWPSRCHFFSYCWLHH 120  
 Qy 121 RFDPKASSSTQANGTKFAQYGTGRDGLSEDKLUTIGKKGASVIFGRALWEISLVAF 180  
 Db 121 RFDPKASSSTQANGTKFAQYGTGRDGLSEDKLUTIGKKGASVIFGRALWEISLVAF 180  
 Qy 181 AHFDGILGIGPFLSVEGVPRPMDDVIEQGLIDKPVSPYLNRDPPEPDGELVLGGSDP 240  
 Db 181 AHFDGILGIGPFLSVEGVPRPMDDVIEQGLIDKPVSPYLNRDPPEPDGELVLGGSDP 240  
 Qy 241 AHYIPPLTFVFPV 252  
 Db 243 AHYIPPLTFVFPV 254  
 Qy 241 AHYIPPLTFVFPV 255  
 Db 241 AHYIPPLTFVFPV 255  
 Search completed: June 2, 2004, 20:19:01  
 Job time : 103.065 secs

**RESULT 15**  
 AAB85539 standard; protein; 262 AA.  
 ID XX  
 AAB85539; XX  
 AC XX  
 DT 25-SEP-2001 (first entry)  
 DE Human secreted protein (clone Id HCME12).  
 KW Secreted protein; immunosuppressive; antiarthritic; antirheumatic;  
 KW anti-proliferative; cytostatic; cardiotonic; vasoropic; cerebroprotective;  
 KW nootropic; neuroprotective; antibacterial; virucide; fungicide; human;  
 KW ophthalmological; gene therapy.  
 XX Homo sapiens.  
 XX Key Location/Qualifiers  
 FH Misc-difference 231  
 FT /note= "Xaa can be any amino acid"  
 PN WO2001155430-A1.  
 XX 02-AUG-2001.  
 XX PP 17-JAN-2001; 2001WO-US001431.  
 PR 31-JAN-2000; 2000US-0179065P.  
 PR 04-FEB-2000; 2000US-0180638P.  
 PR 12-SEP-2000; 2000US-0231968P.  
 XX PA (HUMA-) HUMAN GENOME SCI INC.  
 XX PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Choi GH;  
 PI Olsen HS, Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH;  
 PI Fiscella M, Ni J, Ruben SM, Barash SC;  
 XX WPI: 2001-476220/51.  
 DR N-PSBP; AXH46949.  
 XX 17 isolated nucleic acid molecules encoding human secreted proteins, used  
 PT to preventing, treating or ameliorating a medical condition.  
 XX  
 PS Claim 11: Page 455-456; 482pp; English.

CC The invention provides novel human secreted proteins and polynucleotides  
 CC encoding them. The secreted proteins can be expressed by standard  
 CC recombinant methodology. The secreted proteins and polynucleotides are  
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,  
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can  
 CC also be used in diagnosing a pathologic condition. The antibodies to  
 CC the proteins can also be used in alleviating symptoms associated with the  
 CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme  
 CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or



RESULT 2	
Q32836	PRELIMINARY; PRT; 2109 AA.
ID	PRT; 2109 AA.
AC	PRT; 2109 AA.
Q32836;	PRT; 2109 AA.
CC	PRT; 2109 AA.
DT 01-NOV-1996	(TREMBLrel. 01, Created)
DT 01-OCT-2003	(TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)
DR ORF2280.	
OS <i>Palargonium horrorum</i> (Common geranium).	
Chloroplst.	
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC Spermatophytina; Magnoliophyta; eudicots; rosids;	
OC Geraniales; Geraniaceae; Perargonium.	
NCBI_TAXID=4031;	
[1]	
SEQUENCE FROM N.A.	
RX MEDLINE=9436755; PubMed=8082181;	
RA Downie S.R., Katz-Downie D.S., Wolfe K.H., Calie P.J., Palmer J.D.;	
PT "Structure and evolution of the largest chloroplast gene (ORF2280): internal plasticity and multiple gene loss during angiosperm evolution."	
RT Curr. Genet. 25:367-378(1994).	
RL DR PIR: T31352; T31352; -.	
DR GO; GO:0009507; C:chloroplast; IEA.	
DR GO; GO:0005524; F:ATP binding; IEA.	
DR GO; GO:000166; F:nucleotide binding; IEA.	
DR InterPro: IPR003593; AAA_ATPase.	
DR InterPro: IPR008543; DUF825.	
DR PFAM: PF00656; DUF825; 1.	
DR SMART; SM00382; AAA; 1.	
KW ATP-binding; Chloroplast.	
SQ SEQUENCE 2109 AA; 245645 MW; 948980477223DE8C CRC64;	
Query Match Best Local Similarity 17.1%; Score 78.5%; DB 8; Length 2109;	
Matches 23; Conservative 16; Mismatches 24; Indels 33; Gaps 3;	
Qy 7 FILVITSLCSYATFLINKVPLPVDFKLAPLPLDNILPFM-----46	
Db 564 FELVLRSLFLYKSLPFLSKPLLSKLI-PLLYSKVLPLSLLSKLIPFFVSCGNIPTHRSE 622	
RESULT 3	
Q98TYS	PRELIMINARY; PRT; 1490 AA.
ID	PRT; 1490 AA.
AC	PRT; 1490 AA.
Q98TYS;	PRT; 1490 AA.
CC	PRT; 1490 AA.
DT 01-JUN-2001	(TREMBLrel. 17, Created)
DT 01-JUN-2001	(TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003	(TREMBLrel. 25, Last annotation update)
DE Cystic fibrosis transmembrane conductance regulator I.	
Salmo salar (Atlantic salmon).	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
Actinopterygii; Neopterygii; Teleostei; Euteleostei;	
Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.	
NCBI_TAXID=8030;	
[1]	
SEQUENCE FROM N.A.	
RA Chen J., Jacques C., Mercier B., Boeuf G., Ferec C.;	
RT "Salmo salar cystic fibrosis transmembrane conductance regulator I.";	
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.	
-!- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.	
EMBL: AF319595; AAK07405.1; -.	
DR GO; GO:0016021; C:integral to membrane; IEA.	
DR GO; GO:0005524; F:ATP binding; cassette (ABC) transporter acti. . . IEA.	
DR GO; GO:0004009; F:nucleotide binding; IEA.	
DR InterPro: IPR003593; AAA_ATPase.	
DR InterPro: IPR008543; ABC_TRANSPORTER_1;	
DR InterPro: IPR005591; CFTR_protein; 1.	
DR PROSITE; PS00211; ABC_TRANSPORTER_1;	
KW ATP-binding; Transmembrane; Transport.	
SQ SEQUENCE 1519 AA; 171239 MW; F4467DF228988240C CRC64;	
Query Match Best Local Similarity 16.7%; Score 76.5%; DB 13; Length 1519;	
Matches 28; Conservative 10; Mismatches 24; Indels 15; Gaps 3;	
DR InterPro: IPR003593; AAA_ATPase.	
DR InterPro: IPR00654; ABC_membrane; 2.	
DR ProDom; PD000006; ABC_tran; 2.	
DR SMART; SM0032; AAA; 2.	
DR TIGRFAMS; TIGR0953; 3a01202; 1.	
DR PROSITE; PS00211; ABC_TRANSPORTER_2;	
KW ATP-binding; Transmembrane; Transport.	

QY	31 VDKLAPLPLDNLIPFMDP--IKLLIKTLG-----ISVEHLVVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DB	1395 LSKARIILIDDEPSAFLDPTLQLVRKTLIQGSFSNCTVILSEHRTVPELLEQCSFLM <span style="color:red">IEKS</span> 1454		DE Glutamine synthetase, probable.
QY	80 ---EAVKKLEALSHL 92		GN 1M97.
DB	1455 MKRVDISIQLNNETSHL 1471		OS Cryptosporidium parvum.
	SEQUENCE FROM N.A.		OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Bimerida;
	RC STRAIN=Iowa;		OC Cryptosporidiidae; Cryptosporidium.
	RA Barkier A.T.; Spriggs H.F.; Furtmann B.; Konfortov B.A.; Madera M.,		NCBI_TAXID=5407;
	RA Vogel C.; Teichmann S.A.; Ivens A.; Dear P.H.;		RN [1]
	RT "Integrated mapping, chromosomal sequencing and sequence analysis of		RP SEQUENCE FROM N.A.
	RL Genome Res. 0:0-0(2003);		RC
	DR EML; BX53853; CAD98273.1; -.		RA
	SQ D7BEAB422FA18886 CRC64;		RT
	SEQUENCE 481 AA; 54314 MW;		RT Cryptosporidium parvum."
	Query Match 16.0%; Score 73.5; DB 5; Length 481;		RL
	Best Local Similarity 24.4%; Pred. No. 23;		DR
	Matches 19; Conservative 18; Mismatches 32; Indels 9; Gaps 1;		DR
	QY 23 LINKVLPFLVDKLAPLPLDNLIPFMDPKLKLTGIGSVEHLVVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 186 LASRPRPKQAYCAPYPVDRDLURSEILEDENINGTVKEHHHEVATCQHEIGVHCS <span style="color:red">TLV</span> 245		DR
	QY 80 -----EAVKKLEALSHL 91		DR
	Db 246 QSDADIVESIRYLIKGI <span style="color:red">AH</span> 263		DR
	SEQUENCE FROM N.A.		DR
	RY MEDLINE=98191134; PubMed=9530103;		DR
	RA Singer T.D.; Tucher S.J.; Marshall W.S.; Higgins C.F.;		DR
	RT "A divergent CTRP homologue: highly regulated salt transport in the		DR
	RT euryhaline teleost fish heteroclitus."		DR
	RL Am. J. Physiol. 274:C715-C723(1998).		DR
	CC ! SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		DR
	DR EMBL; AF00271; AAC1271.1; -.		DR
	DR GO; GO:0016021; C:integral to membrane; IEA.		DR
	DR GO; GO:0005524; F:ATP binding; IEA.		DR
	DR GO; GO:00409; F:ATP-binding cassette (ABC) transporter acti.. . ; IEA.		DR
	DR GO; GO:000166; F:nucleotide binding; IEA.		DR
	DR InterPro; IPR003593; AAA ATPase.		DR
	DR InterPro; IPR001140; ABC TM transprt.		DR
	DR InterPro; IPR003439; ABC transporter.		DR
	DR InterPro; IPR005291; CAMP_G1_channel.		DR
	PFam; PF00664; ABC membrane; 2.		DR
	PFam; PF00005; ABC_tran; 2.		DR
	ProDom; PD00006; ABC transporter; 2.		DR
	SMART; SM0382; AAA; 2.		DR
	TIGRFAMS; TIGR00953; 3a01202; 1.		DR
	TIGRFAMS; TIGR01271; CFTR_protein; 1.		DR
	PROSITE; PS00211; ABC TRANSPORTER_1; 1.		DR
	PROSITE; PS50892; ABC TRANSPORTER_2; 2.		DR
	KW ATP-binding; Transmembrane Transporter.		DR
	SQ SEQUENCE 1503 AA; 169250 MW; B95766EEFA205920 CRC64;		DR
	Query Match 16.4%; Score 75.5; DB 13; Length 1503;		DR
	Best Local Similarity 35.1%; Pred. No. 45;		DR
	Matches 27; Conservative 14; Mismatches 21; Indels 15; Gaps 4;		DR
	QY 31 VDKLAPLPLDNLIPFMDP--IKLLIKTLG-----GISV---BHLVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 1379 LSKARIILIDDEPSAFLDPTLQLVRKTLIQGSFSNCTVILSEHRTVPELLEQCSFLM <span style="color:red">IEKS</span> 1438		DR
	QY 80 ---EAVKKLEALSHL 92		DR
	Db 1439 VKSYDSIQLNNEMSHL 1455		DR
	SEQUENCE FROM N.A.		DR
	RC STRAIN=Iowa;		DR
	RA Barkier A.T.; Spriggs H.F.; Furtmann B.; Konfortov B.A.; Madera M.,		DR
	RA Vogel C.; Teichmann S.A.; Ivens A.; Dear P.H.;		DR
	RT "Integrated mapping, chromosomal sequencing and sequence analysis of		DR
	RL Genome Res. 0:0-0(2003);		DR
	DR EML; BX53853; CAD98273.1; -.		DR
	SQ D7BEAB422FA18886 CRC64;		DR
	SEQUENCE 481 AA; 54314 MW;		DR
	QY 23 LINKVLPFLVDKLAPLPLDNLIPFMDPKLKLTGIGSVEHLVVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 186 LASRPRPKQAYCAPYPVDRDLURSEILEDENINGTVKEHHHEVATCQHEIGVHCS <span style="color:red">TLV</span> 245		DR
	QY 80 -----EAVKKLEALSHL 91		DR
	Db 246 QSDADIVESIRYLIKGI <span style="color:red">AH</span> 263		DR
	SEQUENCE FROM N.A.		DR
	RY MEDLINE=98191134; PubMed=9530103;		DR
	RA Singer T.D.; Tucher S.J.; Marshall W.S.; Higgins C.F.;		DR
	RT "A divergent CTRP homologue: highly regulated salt transport in the		DR
	RT euryhaline teleost fish heteroclitus."		DR
	RL Am. J. Physiol. 274:C715-C723(1998).		DR
	CC ! SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		DR
	DR Q9IAR8; PRELIMINARY; PRT; 1518 AA.		DR
	AC Q9IAR8; PRELIMINARY; PRT; 1518 AA.		DR
	DT 01-OCT-2000 (TREMBLrel. 15, Created)		DR
	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		DR
	DT 01-DEC-2003 (TREMBLrel. 15, Last annotation update)		DR
	DE Cystic fibrosis transmembrane conductance regulator II.		DR
	DR Salmo salar (Atlantic salmon).		DR
	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		DR
	OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;		DR
	OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.		DR
	NCBI_TAXID=8030;		DR
	RN [1] SEQUENCE FROM N.A.		DR
	RP MBDLINE=2139640; PubMed=11504857;		DR
	RA Chen J.M.; Cutler C.; Jacques C.; Boef G.; Denamur E.; Lecointre G.,		DR
	RA Mercier B.; Cramb G.; Perez C.,		DR
	RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance Regulator: Implications for Structure and Disease Models."		DR
	RL Mol. Biol. Evol. 18:1771-1788(2001).		DR
	CC !:SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		DR
	DR EMBL; AF161070; AAF37801.1; -.		DR
	DR GO; GO:0016021; C:integral to membrane; IEA.		DR
	DR GO; GO:0005524; F:ATP binding; IEA.		DR
	DR InterPro; IPR003593; AAA ATPase.		DR
	DR InterPro; IPR001140; ABC TM transport.		DR
	DR InterPro; IPR003439; ABC transporter.		DR
	DR InterPro; IPR005291; CAMP_G1_channel.		DR
	PFam; PF00664; ABC membrane; 2.		DR
	ProDom; PD00006; ABC transporter; 2.		DR
	SMART; SM00382; AAA; 2.		DR
	TIGRFAMS; TIGR00953; 3a01202; 1.		DR
	DR TIGRFAMS; TIGR01271; CFTR_protein; 1.		DR
	DR PROSITE; PS00211; ABC TRANSPORTER_1; 1.		DR
	DR PROSITE; PS50892; ABC TRANSPORTER_2; 2.		DR
	KW ATP-binding; Transmembrane Transporter.		DR
	SQ SEQUENCE 1503 AA; 169250 MW; B95766EEFA205920 CRC64;		DR
	Query Match 16.4%; Score 75.5; DB 13; Length 1503;		DR
	Best Local Similarity 35.1%; Pred. No. 45;		DR
	Matches 27; Conservative 14; Mismatches 21; Indels 15; Gaps 4;		DR
	QY 31 VDKLAPLPLDNLIPFMDP--IKLLIKTLG-----GISV---BHLVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 1379 LSKARIILIDDEPSAFLDPTLQLVRKTLIQGSFSNCTVILSEHRTVPELLEQCSFLM <span style="color:red">IEKS</span> 1438		DR
	QY 80 ---EAVKKLEALSHL 92		DR
	Db 1439 VKSYDSIQLNNEMSHL 1455		DR
	SEQUENCE FROM N.A.		DR
	RC STRAIN=Iowa;		DR
	RA Barkier A.T.; Spriggs H.F.; Furtmann B.; Konfortov B.A.; Madera M.,		DR
	RA Vogel C.; Teichmann S.A.; Ivens A.; Dear P.H.;		DR
	RT "Integrated mapping, chromosomal sequencing and sequence analysis of		DR
	RL Genome Res. 0:0-0(2003);		DR
	DR EML; BX53853; CAD98273.1; -.		DR
	SQ D7BEAB422FA18886 CRC64;		DR
	SEQUENCE 481 AA; 54314 MW;		DR
	QY 23 LINKVLPFLVDKLAPLPLDNLIPFMDPKLKLTGIGSVEHLVVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 186 LASRPRPKQAYCAPYPVDRDLURSEILEDENINGTVKEHHHEVATCQHEIGVHCS <span style="color:red">TLV</span> 245		DR
	QY 80 -----EAVKKLEALSHL 91		DR
	Db 246 QSDADIVESIRYLIKGI <span style="color:red">AH</span> 263		DR
	SEQUENCE FROM N.A.		DR
	RY MEDLINE=98191134; PubMed=9530103;		DR
	RA Singer T.D.; Tucher S.J.; Marshall W.S.; Higgins C.F.;		DR
	RT "A divergent CTRP homologue: highly regulated salt transport in the		DR
	RT euryhaline teleost fish heteroclitus."		DR
	RL Am. J. Physiol. 274:C715-C723(1998).		DR
	CC ! SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		DR
	DR Q9IAR8; PRELIMINARY; PRT; 1518 AA.		DR
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	DT 01-OCT-2000 (TREMBLrel. 15, Created)		DR
	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		DR
	DT 01-DEC-2003 (TREMBLrel. 15, Last annotation update)		DR
	DE Cystic fibrosis transmembrane conductance regulator II.		DR
	DR Salmo salar (Atlantic salmon).		DR
	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		DR
	OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;		DR
	OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.		DR
	NCBI_TAXID=8030;		DR
	RN [1] SEQUENCE FROM N.A.		DR
	RP MBDLINE=2139640; PubMed=11504857;		DR
	RA Chen J.M.; Cutler C.; Jacques C.; Boef G.; Denamur E.; Lecointre G.,		DR
	RA Mercier B.; Cramb G.; Perez C.,		DR
	RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance Regulator: Implications for Structure and Disease Models."		DR
	RL Mol. Biol. Evol. 18:1771-1788(2001).		DR
	CC !:SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		DR
	DR EMBL; AF161070; AAF37801.1; -.		DR
	DR GO; GO:0016021; C:integral to membrane; IEA.		DR
	DR GO; GO:0005524; F:ATP binding; IEA.		DR
	DR InterPro; IPR003593; AAA ATPase.		DR
	DR InterPro; IPR001140; ABC_TM_transprt.		DR
	DR InterPro; IPR003439; ABC_transporter.		DR
	DR InterPro; IPR005291; CAMP_c1_channel.		DR
	PFam; PF00664; ABC membrane; 2.		DR
	ProDom; PD00006; ABC_transprt.		DR
	SMART; SM00382; AAA; 2.		DR
	TIGRFAMS; TIGR00953; 3a01202; 1.		DR
	DR TIGRFAMS; TIGR01271; CFTR_protein; 1.		DR
	DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.		DR
	DR PROSITE; PS50892; ABC_TRANSPORTER_2; 2.		DR
	KW ATP-binding; Transmembrane Transporter.		DR
	SQ SEQUENCE 1503 AA; 169250 MW; B95766EEFA205920 CRC64;		DR
	Query Match 16.4%; Score 75.5; DB 13; Length 1503;		DR
	Best Local Similarity 35.1%; Pred. No. 45;		DR
	Matches 27; Conservative 14; Mismatches 21; Indels 15; Gaps 4;		DR
	QY 31 VDKLAPLPLDNLIPFMDP--IKLLIKTLG-----GISV---BHLVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 1379 LSKARIILIDDEPSAFLDPTLQLVRKTLIQGSFSNCTVILSEHRTVPELLEQCSFLM <span style="color:red">IEKS</span> 1438		DR
	QY 80 ---EAVKKLEALSHL 92		DR
	Db 1439 VKSYDSIQLNNEMSHL 1455		DR
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	RC STRAIN=Iowa;		DR
	RA Barkier A.T.; Spriggs H.F.; Furtmann B.; Konfortov B.A.; Madera M.,		DR
	RA Vogel C.; Teichmann S.A.; Ivens A.; Dear P.H.;		DR
	RT "Integrated mapping, chromosomal sequencing and sequence analysis of		DR
	RL Genome Res. 0:0-0(2003);		DR
	DR EML; BX53853; CAD98273.1; -.		DR
	SQ D7BEAB422FA18886 CRC64;		DR
	SEQUENCE 481 AA; 54314 MW;		DR
	QY 23 LINKVLPFLVDKLAPLPLDNLIPFMDPKLKLTGIGSVEHLVVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 186 LASRPRPKQAYCAPYPVDRDLURSEILEDENINGTVKEHHHEVATCQHEIGVHCS <span style="color:red">TLV</span> 245		DR
	QY 80 -----EAVKKLEALSHL 91		DR
	Db 246 QSDADIVESIRYLIKGI <span style="color:red">AH</span> 263		DR
	SEQUENCE FROM N.A.		DR
	RY MEDLINE=98191134; PubMed=9530103;		DR
	RA Singer T.D.; Tucher S.J.; Marshall W.S.; Higgins C.F.;		DR
	RT "A divergent CTRP homologue: highly regulated salt transport in the		DR
	RT euryhaline teleost fish heteroclitus."		DR
	RL Am. J. Physiol. 274:C715-C723(1998).		DR
	CC ! SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		DR
	DR Q9IAR8; PRELIMINARY; PRT; 1518 AA.		DR
	AC Q9IAR8; PRELIMINARY; PRT; 1518 AA.		DR
	DT 01-OCT-2000 (TREMBLrel. 15, Created)		DR
	DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)		DR
	DT 01-DEC-2003 (TREMBLrel. 15, Last annotation update)		DR
	DE Cystic fibrosis transmembrane conductance regulator II.		DR
	DR Salmo salar (Atlantic salmon).		DR
	OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		DR
	OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;		DR
	OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.		DR
	NCBI_TAXID=8030;		DR
	RN [1] SEQUENCE FROM N.A.		DR
	RP MBDLINE=2139640; PubMed=11504857;		DR
	RA Chen J.M.; Cutler C.; Jacques C.; Boef G.; Denamur E.; Lecointre G.,		DR
	RA Mercier B.; Cramb G.; Perez C.,		DR
	RT "A Combined Analysis of the Cystic Fibrosis Transmembrane Conductance Regulator: Implications for Structure and Disease Models."		DR
	RL Mol. Biol. Evol. 18:1771-1788(2001).		DR
	CC !:SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.		DR
	DR EMBL; AF161070; AAF37801.1; -.		DR
	DR GO; GO:0016021; C:integral to membrane; IEA.		DR
	DR GO; GO:0005524; F:ATP binding; IEA.		DR
	DR InterPro; IPR003593; AAA ATPase.		DR
	DR InterPro; IPR001140; ABC_TM_transprt.		DR
	DR InterPro; IPR003439; ABC_transporter.		DR
	DR InterPro; IPR005291; CAMP_c1_channel.		DR
	PFam; PF00664; ABC membrane; 2.		DR
	ProDom; PD00006; ABC_transprt.		DR
	SMART; SM00382; AAA; 2.		DR
	TIGRFAMS; TIGR00953; 3a01202; 1.		DR
	DR TIGRFAMS; TIGR01271; CFTR_protein; 1.		DR
	DR PROSITE; PS00211; ABC_TRANSPORTER_1; 1.		DR
	DR PROSITE; PS50892; ABC_TRANSPORTER_2; 2.		DR
	KW ATP-binding; Transmembrane Transporter.		DR
	SQ SEQUENCE 1503 AA; 169250 MW; B95766EEFA205920 CRC64;		DR
	Query Match 16.4%; Score 75.5; DB 13; Length 1503;		DR
	Best Local Similarity 35.1%; Pred. No. 45;		DR
	Matches 27; Conservative 14; Mismatches 21; Indels 15; Gaps 4;		DR
	QY 31 VDKLAPLPLDNLIPFMDP--IKLLIKTLG-----GISV---BHLVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 1379 LSKARIILIDDEPSAFLDPTLQLVRKTLIQGSFSNCTVILSEHRTVPELLEQCSFLM <span style="color:red">IEKS</span> 1438		DR
	QY 80 ---EAVKKLEALSHL 92		DR
	Db 1439 VKSYDSIQLNNEMSHL 1455		DR
	SEQUENCE FROM N.A.		DR
	RC STRAIN=Iowa;		DR
	RA Barkier A.T.; Spriggs H.F.; Furtmann B.; Konfortov B.A.; Madera M.,		DR
	RA Vogel C.; Teichmann S.A.; Ivens A.; Dear P.H.;		DR
	RT "Integrated mapping, chromosomal sequencing and sequence analysis of		DR
	RL Genome Res. 0:0-0(2003);		DR
	DR EML; BX53853; CAD98273.1; -.		DR
	SQ D7BEAB422FA18886 CRC64;		DR
	SEQUENCE 481 AA; 54314 MW;		DR
	QY 23 LINKVLPFLVDKLAPLPLDNLIPFMDPKLKLTGIGSVEHLVVEGLRKCVNELGP <span style="color:red">EAS-</span>	79	DR
	DB 186 LASRPRPKQAYCAPYPVDRDLURSEILEDENINGTVKEHHHEVATCQHEIGVHCS <span style="color:red">TLV&lt;/</span>		



Db	315 FLIVCVSLVSLVANAF----DISKLTPIKEFTRLRLRPLRALSR-----PRG	358	AC Q7XH05; DT 01-OCT-2003 (TREMBrel. 25, Created)
Qy	67 LRKCVNELLGPPASEAVKLLKLEAL 89		DT 01-OCT-2003 (TREMBrel. 25, Last sequence update)
Db	359 MRRVVVNAFFGAIPSTVNLVCL 381		DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)
RESULT 11			DE Putative aldehyde oxidase.
Q8WZP4	PRELIMINARY;	PRT; 1358 AA.	GN OSJUNA008JH07 7.
AC Q8WZP4;			OS <i>Oryza sativa</i> (japonica cultivar-group).
DT 01-MAR-2002 (TREMBrel. 20, Created)			OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
DT 01-OCT-2002 (TREMBrel. 20, Last sequence update)			OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
DT 01-OCT-2003 (TREMBrel. 25, Last annotation update)			OC Ehrhartoideae; Oryzeae; Oryza.
DE Putative aldehyde oxidase.			OC NCBI_TaxID=3947;
OS Oryza sativa (Rice).			RN [1]
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			RP SEQUENCE FROM N.A.
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			RC STRAIN=cv_Nipponbare;
OC Ehrhartoideae; Oryzeae; Oryza.			RA The Rice Chromosome 10 Sequencing Consortium;
OX NCBI_TaxID=4530;			RT "In-depth view of structure, activity, and evolution of rice
RN [1]			RT chromosome 10.";
RP SEQUENCE FROM N.A.			RL science 300:1566-1569 (2003).
RA Wing R.A., Yu Y., Yang T.-J., Nah G., Soderlund C., Chen M., Kim H.-R.,			RN [2]
RA Rambo T., Sasaki C., Henry D., Oates R., Simmons J.,			RP SEQUENCE FROM N.A.
RT "Rice Genomic Sequence."			RC STRAIN=cv_Nipponbare;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.			RA Bue I.C.R., Wing R.A., McCombie W.R., Messing J., Yuan Q.;
DR !- COFACTOR: BINDS 1 to 16 (CLUSTER (BY SIMILARITY).			RA Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
EMBL; AC059733; AL0116-1; -.			DR EMBL; AE017054; AA052052-1; -;
Gramene; Q8WZP4; -.			SQ SEQUENCE 1358 AA; 145452 MW; 75B3A692C75D537D CRC64;
DR GO:0005524; P:ATP binding; IEA.			Query Match 15.4%; Score 70.5; DB 10; Length 1358;
DR GO: GO:0005489; P:electron transporter activity; IEA.			Best Local Similarity 27.9%; Pred. No. 1.4e-02;
DR GO: GO:0016491; P:oxidoreductase activity; IEA.			Matches 24; Conservative 13; Mismatches 38; Indels 11; Gaps 3;
DR GO: GO:004672; P:protein kinase activity; IEA.			Qy 8 LLVTISL---CSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLKTL-GISVEHL 63
DR GO: GO:0006118; P:electron transport; IEA.			Db 407 LLISIISPDWCSDGIFTF-----ETFRRAAPRPGNAVSYVNSAFLARSILDAASGSHL 459
DR GO: GO:0006468; P:protein amino acid phosphorylation; IEA.			Qy 64 VEGLRKCVNELGPSEASEAVKLLKLEAL 89
DR InterPro; IPRO02484; 2Fe-2S bind.			Db 460 IEDVRLAFGAFGSEHAIRASKVEEFL 485
DR InterPro; IPRO005058; 2Fe2S_Fd BS.			RESULT 13
DR InterPro; IPRO005274; Aldkan_dh_bind.			Q9LVPS3
DR InterPro; IPRO00674; Aldkan_dh_hamm.			ID Q9LVPS3
DR InterPro; IPRO005107; CO deh_flav C.			AC Q9LVPS3;
DR InterPro; IPRO02346; dehydrog_molyb.			DT 01-OCT-2000 (TREMBrel. 15, Created)
DR InterPro; IPRO01041; Ferredoxin.			DT 01-OCT-2000 (TREMBrel. 15, Last sequence update)
DR InterPro; IPRO00719; Prot_kinase.			DT 01-OCT-2000 (TREMBrel. 15, Last annotation update)
DR Pfam; PF01315; Ald_Xan_dh_C; 1.			DE Genomic DNA, chromosome 3, P1 clone: MME2.
DR Pfam; PF02738; Ald_Xan_dh_C2; 1.			OS Arabidopsis thaliana (Mouse-ear cress).
DR Pfam; PF03440; CO_deh_Flav_C; 1.			OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
DR Pfam; PF00941; FAD_binding_5; 1.			OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
DR Pfam; PF00111; fer2; 1.			OC euroids II; Brassicales; Brassicaceae; Arabidopsis.
DR Prodrom; PD186071; 2Fe-2S bind; 1.			DR NCBI_TaxID=3702;
DR PROSITE; PS00197; 2FE2S_FERREDOXIN_1.			RN [1]
DR PROSITE; PS00101; PROTEIN_KINASE_ATP; 1.			RP SEQUENCE FROM N.A.
KW Iron; Iron-sulfur.			RC STRAIN=Columbia;
SEQUENCE 1358 AA; 145453 MW; 75B3A692C75D537D CRC64;			RA Satoh S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;
Query Match 15.4%; Score 70.5; DB 10; Length 1358;			RA Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
Best Local Similarity 27.9%; Pred. No. 1.4e+02;			RL RN [2]
Matches 24; Conservative 13; Mismatches 38; Indels 11; Gaps 3;			RP SEQUENCE FROM N.A.
Qy 8 LLVTISL---CSYSATAFLINKVPLPVDKLAPLPLDNILPFMDPLKLKTL-GISVEHL 63			RC STRAIN=Colombia;
Db 407 LLISIISPDWCSDGIFTF-----ETFRRAAPRPGNAVSYVNSAFLARSILDAASGSHL 459			RX MEDLINE=20777480; PubMed=10819329;
Qy 64 VEGLRKCVNELGPSEASEAVKLLKLEAL 89			RA Nakamura Y.;
Db 460 IEDVRLAFGAFGSEHAIRASKVEEFL 485			RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones";
RESULT 12			RL DNA Res. 7:131-135 (2000).
Q7XH05	PRELIMINARY;	PRT; 1358 AA.	DR EMBL; AB018121; BAB01992.1; -;
ID Q7XH05			SQ SEQUENCE 106 AA; 115452 MW; 6AE232BF4C5DODD CRC64;
Query Match 15.3%; Score 70; DB 10; Length 106;			Query Match 15.3%; Score 70; DB 10; Length 106;
Best Local Similarity 27.3%; Pred. No. 11;			Best Local Similarity 27.3%; Pred. No. 11;
Matches 21; Conservative 16; Mismatches 32; Indels 8; Gaps 2;			Matches 21; Conservative 16; Mismatches 32; Indels 8; Gaps 2;





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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC -----  
 CC EMBL: AF313455; AAH24232; AAH24231; -;  
 DR Genew; HGNC:18391; SCGB3A2.  
 DR MIM: 606531; -.  
 DR KW SIGNAL. 1 21 POTENTIAL.  
 FT SIGNAL 1 93 UTEROGLOBIN-RELATED PROTEIN 1.  
 FT CHAIN 22 93  
 SEQUENCE 93 AA: 10161 MW: FBD4BFAC2BF3718 CRC64;  
 QC Query Match 100.0%; Score 459; DB 1; Length 93;  
 QC Best Local Similarity 100.0%; Pred. No. 1e-31;  
 QC Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QC Sequence 93 AA:  
 QC 1 MKLVTFILVITISLCSYSATAFLINKPVLDKLAPEILDNLDPMDKLKLTKLGCSV 60  
 QC 1 MKLVTFILVITISLCSYSATAFLINKPVLDKLAPEILDNLDPMDKLKLTKLGCSV 60  
 DB Db 61 EHLVEGRLRKCYNELGPASEAIVEAKLLEAISHLV 93  
 QC Qy 61 EHLVEGRLRKCYNELGPASEAIVEAKLLEAISHLV 93  
 DB Db 61 EHLVEGRLRKCYNELGPASEAIVEAKLLEAISHLV 93  
 QC  
 RESULT 2  
 UGR1\_MOUSE  
 ID UGR1\_MOUSE STANDARD; PRT; 139 AA.  
 AC Q920H1; OS920H2; Q920H3;  
 DT 28-FEB-2003 (Rel. 41; Created)  
 DT 28-FEB-2003 (Rel. 41; Last sequence update)  
 DT 28-FEB-2003 (Rel. 41; Last annotation update)  
 DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A  
 DE member 2).  
 SCGB3A2 OR UGR1P1.  
 OS Mus musculus (Mouse).  
 OC Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Butcharia; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TAXID=10090;  
 RN [1]  
 SEQENCE FROM N.A. (ISOFORMS A; B AND C).  
 RC TISSUE=Lung;  
 RX MEDLINE=21539178; PubMed=11682631;  
 RA Nimi T.; Keck-Waggoner C.L.; Popescu N.C., Zhou Y., Levitt R.C.,  
 RA Kimura S.;  
 RT "UGR1, a uteroglobin/clara cell secretory protein-related protein, is  
 a novel lung-derived downstream target gene for the T/BP/NRX2.1  
 homeodomain transcription factor.";  
 RT Mol. Endocrinol. 15:2021-2036 (2001).  
 RL -  
 RT SUBCELLULAR LOCATION: Secreted.  
 CC -  
 CC -  
 CC -  
 CC Event-Alternative PRODUCTS:  
 CC Name=C;  
 CC IsoID=Q920H1-1; Sequence=Displayed;  
 CC Name=A;  
 CC IsoID=Q920H1-2; Sequence=VSP\_006727; VSP\_006728;  
 CC Name=B;  
 CC IsoID=Q920H1-3; Sequence=VSP\_006726;  
 CC -  
 CC TISSUE SPECIFICITY: Highly expressed in lung.  
 CC -  
 CC SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.  
 CC -----  
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CC -----  
 CC EMBL: AF274950; AAL25701; -;  
 DR EMBL: AF274960; AAL25709; -;  
 DR EMBL: AF274970; AAL25710; -;

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CC	DR GO; GO:0005125; P:cytokine activity; NAS.
CC	DR GO; GO:0030308; P:negative regulation of cell growth; NAS.
CC	DR MGD; MGI:1915912; Scgb3al.
KW	Cytokine; Signal.
FT	POTENTIAL.
FT	CHAIN 22 104 UTEROGLOBIN-RELATED PROTEIN 2.
FT	SEQUENCE 104 AA; 10591 MW; D62F0E601FB57A6D CRC64;
Query Match	Score 35.4%; Score 162.5%; DB 1; Length 104;
Best Local Similarity 40.0%; Pred. No. 1..1e-09;	
Matches 42; Conservative 17; Mismatches 27; Indels 19; Gaps 3;	
Qy	1 MKLVTIFILVTLISLCSYSATFLINKVPL---PVDKIAP -LPLDNTLPF 45
Db	1 MKLTTTFLVCLVALLSDSGVAFMDSLAKPAVEPVAAIAAEAVAGAVSPSLPLSHIA-- 58
Qy	46 MDPLKLUKTKLGSVVEHLVLRKCYNELGPEASEAYKKJLEALS 90
Db	59 -- ILRFLIASMGIPLDLPIEGSRKCVTELGPGEAVGAVRSLLAVLT 101
RESULT 4	UGR2_HUMAN
ID	UGR2_HUMAN STANDARD; PRT; 104 AA.
AC	Q96QR1; Q96PL0;
DT	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in normal-1) (Secretoglobin family 3A member 1).
DE	SCGB2A1 OR UGRP2 OR HIN1.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
RN	SEQUENCE FROM N.A. MEDLINE=99167354; PubMed=100666439;
RX	Zhao C.; Nguyen T.; Yusifov T.; Lehrer R.I.; LeBlanc B.J.; Glasgow B.J.; Lehrer R.I.;
RA	"Lipophilin": human peptides homologous to rat prostatein.";
RA	Kaelin C.M., Rhein E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyzak K.,
RA	"HIN-1", a putative cytokine highly expressed in normal but not cancerous mammary epithelial cells"; Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
RN	SEQUENCE FROM N.A. MEDLINE=21396515; PubMed=11481438;
RX	Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.,
RA	"UGRP1, a uteroglobin/clara cell secretory protein-related protein, is a novel lung enriched downstream target gene for the T/EBP/NKX2.1 homeodomain transcription factor." Mol. Endocrinol. 15:2021-2036(2001).
RT	- FUNCTION: Potential growth inhibitory cytokine.
CC	-- SUBCELLULAR LOCATION: Secreted.
CC	-- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in breast cancer cell lines.
CC	-- SIMILARITY: Belongs to the uteroglobin family. UGRRP subfamily.
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EMBL	AY00564; AAK2942.1; -;
EMBL	AE33458; AAL26217.1; -;
DR	Gene: HGNC:18384; SCGB3A1.
DR	MIM: 606500; -
DR	GO; GO:005576; C:extracellular; NAS.
RESULT 5	GPPB_HUMAN
ID	GPPB_HUMAN STANDARD; PRT; 90 AA.
AC	Q95969;
DT	30-MAY-2000 (Rel. 39, Created)
DT	30-MAY-2000 (Rel. 39, Last sequence update)
DT	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Lipophilin B precursor (Secretoglobin family 1D member 2).
GN	SCGB1D2 OR LIPHOB.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC	NCBI_TaxID=9606;
RN	SEQUENCE FROM N.A. MEDLINE=99167354; PubMed=100666439;
RX	Rhee E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z., Belina D., Razumovic J., Polyzak K.,
RA	"Lipophilin": human peptides homologous to rat prostatein.";
RA	Biochem. Biophys. Res. Commun. 256:147-155(1999).
RA	- FUNCTION: May bind androgens and other steroids, may also bind estramustine, a chemotherapeutic agent used for prostate cancer.
CC	CC MAY BE UNDER TRANSCRIPTIONAL REGULATION OF STEROID HORMONES.
CC	-- SUBCELLULAR LOCATION: Secreted (Potential).
CC	-- TISSUE SPECIFICITY: Highest expression was found in skeletal muscle. Expressed as well in thymus, trachea, kidney, steroid responsive tissues (prostate, testis, uterus, breast and ovary), and salivary gland.
CC	-- SIMILARITY: Belongs to the uteroglobin family. Lipophilin subfamily.
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CC	EMBL; AJ224172; CAA11864.1; -;
DR	Genew: HGNC:18316; SCGB1D2.
DR	GO; GO:0005615; C:extracellular space; TAS.
DR	InterPro; IPR00329; Uteroglobin_sub1.
DR	InterPro; IPR00038; Uteroglobin_sub2.
DR	PFAM; PF01099; Uteroglobin_1.
DR	PRINTS; PRO0486; UTEROGLOBIN.
KW	POTENTIAL.
FT	SIGNAL 1 21 LIPOPHILIN B.
FT	CHAIN 22 90 LIPOPHILIN B.
FT	SEQUENCE 90 AA; 9925 MW; 17BB55ED035D1AF CRC64;
Query Match	Score 75.5%; DB 1; Length 90;

Best Local Similarity 27.0%; Pred. No. 0.57; Mismatches 18; Indels 34; Gaps 5;

Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

QY 1 MKLTVIFLVITISOSYSATAFLINKVLPDKLAPLPLDNILPFM---DPL-KLLKTL 56

DB :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| 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RESULT 6

YF09\_METJIA STANDARD PRT; 153 AA.

DB 57 GISVHLVE-GLRKCCNLGPE---ASEAVKKELEA 90

50 DAPPEAAAKLGVRKCTDMSLQRSLIAEVLKILKCS 89

RP SEQUENCE FROM N.A.

STRAIN=CPR06; PubMed=28266688;

AC Q58904; RA 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DB 16-OCT-2001 (Rel. 40, Last annotation update)

GN M0109.

OS Methanococcus jannaschii

OC Archaea; Euryarchaeota; Methanococcales;

OC Methanococcoides; Methanococcaceae; Methanococcoides

OX RT SEQUENCE FROM N.A.

RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

RA Built C.J., White O., Olsen G.J., Fleischmann R.D., Kerlavage A.R., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D., Overbeek R., Dougherty B.A., Tomb J.F., Adams M.D., Reich C.I., Merrick J.M., Glodek A., Scott J.L., Geoghegan N.S.M., Weidman J.D., Fuerstmann D., Utterback T.R., Kelley J.M., Peterman J.D., Sadow P.W., Hanna M.C., Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M., Klene H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; RT PIR; DR TIGR; MJL509; D64488.

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CC DR U67592; AAB9934.1; DR PIR; DR TIGR; MJL509; D64488.

CC Hypothetical protein; Complete proteome.

SQ SEQUENCE 153 AA; 17718 MW; OBIABEDC831685B CRC64;

Query Match 15.7%; Score 72; DB 1; Length 153;

Matches 19; Conservative 28.8%; Pred. No. 2.2; Mismatches 22; Indels 8; Gaps 2;

QY 22 FLINKVLPDKLAPLPLDNILPFMDEKLKLTGIGSVHLVEGLRKCYNGLPESEA 81

DB 93 YMKKCLP-----GDLPLDDIV--VNLPLPLTTVGRVTKALHEDIERKEHIEE 144

QY 82 VVKLLE 87

DB 145 AKKVLD 150

Query Match 14.9%; Score 68.5; DB 1; Length 1284;

Best Local Similarity 36.0%; Pred. No. 45; Mismatches 7; Indels 17; Gaps 5;

MatcheB 27; Conservative 24; Mismatches 24;

QY 30 PVDKLAPLPLDNILPFMDEKLKLTGIGSVHLVEGLRKCYNGLPESEA 81

DB 364 PVRVQSKPDGIPYNFPEDPVTPITKVLGTDQVNLVLLIEWLDKCBECGNNG 423

QY 76 ---PEASEAVKKLLE 87

DB 424 EYKTELEEARKLT 438

RESULT 7

ATI\_COWPX STANDARD PRT; 1284 AA.

ID\_ATI\_COWPX P16602; DT 01-AUG-1990 (Rel. 15, Created)

RESULT 8

RPC\_BPPH1 ID\_RPC\_BPPH1 STANDARD PRT; 144 AA.

AC P06153; P15239; 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 01-APR-1990 (Rel. 14, Last annotation update)  
 DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 OS Immunity repressor protein.  
 OS Bacteriophage phi-105.  
 OC Virus; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC Lambda-like viruses.  
 NCBI\_TaxID=10717;  
 RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=82283656; PubMed=3135184;  
 RA van Kaer L., Ganssmuller Y., van Montagu M., Dhaese P.;  
 RT "Interaction of the *Bacillus subtilis* phage phi 105 repressor DNA: a  
 generic analysis";  
 RL EMBO J. 17:859-866 (1998).  
 RN [2] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=85297750; PubMed=2993999;  
 RA Dhaese P., Seurinck J., de Smet B., van Montagu M.;  
 RT "Nucleotide sequence and mutational analysis of an immunity repressor  
 gene from *Bacillus subtilis* temperate phage phi 105.";  
 RL Nucleic Acids Res. 13:5441-5455(1985).  
 RN [3] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=86156972; PubMed=3934047;  
 RA Cully D.F., Garron A.J.;  
 RT "Nucleotide sequence of the immunity region of *Bacillus subtilis*  
 bacteriophage phi 105: identification of the repressor gene and its  
 mRNA and protein products.,";  
 RL Gene 38:153-164(1985).  
 CC -.- SIMILARITY: Contains 1 HTH cro/C1-type DNA-binding domain.  
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 or send an email to license@isb-sib.ch).

CC EMBL; X02799; CHA26567.1; ALT\_INIT.  
 CC InterPro: IPR01387; HTH\_3.  
 DR PFam: PF01181; HTH\_3; 1.  
 DR SMART; SM0530; HTH\_XRE; 1.  
 DR PROSITE; PS00943; HTH\_CRO1; 1.  
 KW Transcription regulation; Repressor; DNA-binding; Early protein.  
 FT DOMAIN 7 61 HTH CRO1-TYPE.  
 FT DOMAIN 18 37 H-T-H MOTIF (POTENTIAL).  
 SQ SEQUENCE 144 AA; 16520 MW; EEDG6B3E4B34ALE CRC64;  
 Best Local Similarity 24.3%; Pred. No. 5.3%; Mismatches 13; Indels 32; Gaps 2;

Query Match 14.8%; Score 68; DB 1; Length 144;  
 Best Local Similarity 24.3%; Pred. No. 5.3%; Mismatches 13; Indels 32; Gaps 2;

Qy 23 LINKVPLPVDKIAPLPLUNILPMDPKKLLTKLGISLEHLY-----64  
 DB 21 LAERANLRSYSLADIERDRYNPLSITAVAGALGIVSAIVGETLKEQAENYSKEE 80

Qy 65 -----EGLRKCVNELG-----PEASEAVKCLLLEALSHLV 93  
 DB 81 KDTAKRMFPIRKOLEKSGLSFSCEPMQEAESLMEAMEHTV 123

RESULT 9  
 SYFB\_HELPJ STANDARD; PRT; 764 AA.  
 ID SYFB\_HELPJ  
 AC Q9JKF8;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)  
 DE (Phenylalanine--tRNA ligase beta chain) (PhERS).  
 GN PHE" OR JHP0979.  
 OS Helicobacter pylori J99 (Campylobacter pylori J99).  
 OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;  
 OC Helicobacteraceae; Helicobacter; Campylobacter.  
 OC NCBITaxonID=85863;  
 OX RN [1] SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=99120557; PubMed=9923682;  
 RA Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig B.C.,  
 RA Smith D.R., Noonan B., Guild B.C., de Jonge B.L., Carmel G.,  
 RA Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,  
 RA Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,  
 RA Trust T.J.;  
 RT "Genomic sequence comparison of two unrelated isolates of the human  
 gastric pathogen *Campylobacter pylori*.";  
 RL Nature 397:176-180(1999).  
 CC -!- CATALYTIC ACTIVITY: ATP + L-phenylalanine + tRNA(Phe) = AMP +  
 CC diphosphate + L-phenylalanyl-tRNA(Phe).  
 CC -!- COFACTOR: Binds 2 magnesium ions on its tetramer (BY similarity).  
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (BY similarity).  
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -!- SIMILARITY: Belongs to the phenylalanyl-tRNA synthetase beta chain  
 CC family. Subfamily 1.  
 CC -!- SIMILARITY: Contains 1 tRNA-binding domain.  
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 CC EMBL; AE001527; AAC06558.1; -.  
 DR PIR; P71863; P71863.  
 DR HAMAP; MP\_00283; -; 1.  
 DR InterPro; IPR005146; B3\_4.  
 DR InterPro; IPR005147; B5\_4.  
 DR InterPro; IPR005121; Fdx\_AntiCB.  
 DR InterPro; IPR008994; Nucleic\_acid\_OB.  
 DR InterPro; IPR004532; Phet\_bact.  
 DR InterPro; IPR004547; tRNA\_bind.  
 DR Pfam; PF03483; B3\_4; 1.  
 DR Pfam; PF03484; B5\_1.  
 DR Pfam; PF03447; FDX\_AcB; 1.  
 DR Pfam; PF01588; tRNA\_bind; 1.  
 DR TIGREAMS; TIGR00472; pher\_bact; 1.  
 DR PROSITE; PS50886; TRBD; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Metal-binding; Magnesium; RNA-binding; tRNA-binding;  
 KW Complete proteome.  
 FT DOMAIN 38 148 TRNA-BINDING.  
 FT METAL 433 433 MAGNESIUM (BY SIMILARITY).  
 FT METAL 439 439 MAGNESIUM (VIA CARBONYL OXYGEN)  
 FT METAL 442 442 MAGNESIUM (BY SIMILARITY).  
 FT METAL 443 443 MAGNESIUM (BY SIMILARITY).  
 SQ SEQUENCE 764 AA; 85154 MW; 70BDADF202FED425 CRC64;  
 Query Match 14.7%; Score 67.5; DB 1; Length 764;  
 Best Local Similarity 38.0%; Pred. No. 33; Indels 7; Gaps 4;  
 Matches 27; Conservative 10; Mismatches 27;

Qy 20 TAFLINKVPLPVDKIAPLPLUNILPMDPKKLLTKLGISLEHLYEGLRKCVNELGPEA 78  
 DB 690 TAAKIKKAL--KDAQIPNLSEILP-LDIFKESGNTIALSVCIHSLEKTLNDD-EEV 743

Qy 79 SEAVKKLLEAL 89  
 DB 744 NSAVQKALEIL 754



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Brownstein M.J., Usdin T.B., Yoshiaki S., Carnici P., Prange C., Raha S.S., Loquai N.A., Peters G.J., Abramson R.D., Mullahay S.J., Bosak S.A., McIwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Holt E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smilus D.E., Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences"; *Nature*, **423**: 652-657; *Sci. & Eng.*, **19**: 11-12; *Proc. Natl. Acad. Sci. U.S.A.*, **99**: 16899-16903 (2002).

	Query	Match	Score	DB	Length	6;
W	Peptidoglycan synthesis; Cell wall; Cell division; Ligase;					
W	ATP-binding; Complete proteome.					
T	NP BIND	111 117	ATP (POTENTIAL)			
T	SEQUENCE	445 AA;	B9CCCF437FBAA6 CRC64;			
Q	50129 MW;					
Y	Query Match	14 6%;	Score 67;	DB 1;	Length 445;	
Y	Best Local Similarity	32.0%;	Pred. No. 22;			
Y	Matches 31;	Conservative 12;	Mismatches 24;	Indels 30;	Gaps 6;	
Y						
b	6 IFLIV ---TISLCSYSATAFLINKVPLPVDFKLAIPDLDNILPFMDPLKLLKTIGISVE 61					
b	221 IFVLLORDQSIRKLIPPSVTKLNGISIVDDRIH ---DNLDITYKLPLN --KNI---					268
Y	62 HLVEGLRKCYNNEGLPRAEAV --- -KYLLEAIS 90					
b	269 ---QGIDNCEN --TANSYAYAKIGLESKKKILEIS 299					

RESULT 12		CLUSTER HUMAN D	STANDARD; C9UCM2; Q9UCM4; 01-OCT-1989 (Rel. 12, Created)	FRT;	91 AA.
C					10-Oct-1989 (Rel. 12, Last sequence update)
T					10-Oct-2003 (Rel. 42, Last annotation)
T					Clara cell phospholipid-binding protein Precorbin (CCPB) (Clara cells clara-cell-phospholipid-binding-protein-precorbin (CCPB) (microprotein 1) clara-cell-phospholipid-binding-protein-precorbin (CCPB) (microprotein 1)

U XIA SECRETARY PROLURE (U.S.) (U.S. GOVERNMENT -)  
UPL. SCGB1A1 OR UGB OR CC10 OR CCSP.  
IN HOMO sapiens (Human).  
DC BUKARYOTA; METASOA; CHORDATA; CRANIATA; VERTEBRATA; EUTELEOSTOMI;  
MAMMALIA; EUTHERIA; PRIMATES; CATARRHINI; HOMINIDAE; HOMO.  
OC NMIC TAXON-9606.  
OX

[3] Am. J. Physiol. 268:L565-L575 (1995).  
 RNL RN [3]  
 SEQUENCE FROM N.A.  
 TISSUE=pancreas;  
 MEDLINE=223882257; PubMed=12477932;  
 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner L., Schatzman C.M., Bhat N.K., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stanifer M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.



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CC EMBL; U67372; ARB9934.1; -.

CC PIR; H64464; H64464.

DR TIGR; M011321; -.

DR InterPro; IPR003165; Piwi.

PFam; PF02471; Piwi; 1.

DR Hypothetical protein; PS50822; PWi; 1.

KW Hypothetical protein; Complete proteome.

FT DOMAIN 426 699 PIWI.

SEQUENCE 713 AA; 84582 MW; EB0B3265CS600DF2D CRC64;

Query Match 14.5%; Score 66.5%; DB 1; Length 207;

Best Local Similarity 26.2%; Pred. No. 14;

Matches 22; Conservative 13; Mismatches 42; Indels 7; Gaps 2;

Qy 13 SLC35A1AFLINK---VPLPVDFKAPLPLDNILPMDPLKLTKLGISVEHLVGLRK 69

Db 64 SMCHFSSLQIPNDKQDALKVPEDELLSLRSLLAWSPLA---LSSKASSLAAHPERN 119

Qy 70 CYNELGPEASEAVKGKLEALSHLY 93

Db 120 TINSKTKELOQDNINSLVPGLEHVV 143

Search completed: June 2, 2004, 20:19:13

job time : 4.6175 secs

---

RESULT 15

PRL\_HYPMO STANDARD; PRT; 207 AA.

ID PRL\_HYPMO

AC P35395.

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Prolacrin precursor (PRL) (Fragment)

GN PRL.

OS Hypophthalmichthys molitrix (Silver carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;

OC Cyprinidae; Hypophthalmichthys.

OX NCBI\_TaxID=13095;

BN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=pituitary; PubMed=11398019;

RX MEDLINE=93012875;

RA Chang Y.S., Huang F.-L., Lo T.B.;

RT "Molecular cloning of silver carp and bighead carp prolactin.";

RL Gen. Comp. Endocrinol. 87:260-265(1992).

CC -!- SUBCELLULAR LOCATION: Secretoed.

CC -!- TISSUE SPECIFICITY: Pituitary Glands.

CC -!- SIMILARITY: Belongs to the somatotropin/prolactin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

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CC or send an email to license@isb-sib.ch).

CC

DR EMBL; X61052; CAA43386.1; -.

DR PIR; S21965; S21965.

DR HSSE; Q28632; 1AN3.

DR InterPro; IPR001400; Somatotropin.

PFam; PF00103; hormone; 1.

DR PRINTS; PR00836; SOMATOTROPIN.

DR PROSITE; PS00266; SOMATOTROPIN\_1; 1.

DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.

KW Hormone; Pituitary; Signal.

FT NON\_TER 1 1 BY SIMILARITY.

FT SIGNAL <1 20 BY SIMILARITY.

FT CHAIN 21 207 PROLACTIN.

FT DISULFID 66 180 BY SIMILARITY.

FT DISULFID 197 207 BY SIMILARITY.

SEQUENCE 207 AA; 23033 MW; EB302AA6855FC64D CRC64;

GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.							
Copyright							
OM protein - protein search, using sw model							
Run on:	June 2, 2004, 20:14:10 ;	Search time 6.33063 Seconds (without alignments)					
Title:	US-09-700-770-7						
Perfect score:	459						
Sequence:	1 MKLTIIFLVITISLCYSAT.....LGPEASAEAVKKELEALSHLV 93						
Scoring table:	BLOSUM62						
Gapop	10.0	Gapext 0.5					
Searched:	283366 seqs, 96191526 residues						
Total number of hits satisfying chosen parameters:	283366						
Minimum DB seq length:	0						
Maximum DB seq length:	2000000000						
Post-processing: Minimum Match 0%							
Maximum Match 100%							
Listing first 45 summaries							
Database :	PIR_78:*						
	1: pir1:*						
	2: pir2:*						
	3: pir3:*						
	4: pir4:*						
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES	%	Query	Match	Length	DB ID	Description	
Result No.	Score						
-	-	-	-	-	-	-	-
1	78.5	17.1	21.09	2	T31352	hypothetical prote	RESULT 1
2	72	15.7	153	2	D64488	hypothetical prote	T31352
3	70	15.3	1502	2	T48309	hypothetical prote	
4	69.5	15.1	425	2	H90415	hypothetical prote	
5	69.5	15.1	451	2	A96320	probable ABC trans	
6	69.5	15.1	506	2	F85016	probable RING zinc	
7	69.5	15.1	568	2	E97066	membrane associate	
8	68.5	14.9	335	2	D64568	hypothetical prote	
9	68.5	14.9	356	2	D85406	hypothetical prote	
10	68.5	14.9	464	2	T47710	glucuronosyl trans	
11	68.5	14.9	1284	1	WMY2AI	A-type incision P	
12	68	14.8	147	1	RPBBS	immunity repressor	
13	68	14.8	239	2	D70359	conserved hypothetical	
14	68	14.8	693	2	C86364	prote	
15	67.5	14.7	512	2	A86238	protein FlN23_31	
16	67.5	14.7	566	2	AD0816	nitrate/nitrite se	
17	67.5	14.7	764	2	F71863	phenylalanine-tRNA	
18	67	14.6	95	1	BORT3	prostatic steroid-	
19	67	14.6	445	2	A71699	UDP-n-acetylglucuramido	
20	66.5	14.5	91	2	JS0036	Clara cell 10K pro	
21	66.5	14.5	128	2	T15017	hypothetical prote	
22	66.5	14.5	396	2	B43706	nitrogenase cofact	
23	66.5	14.5	713	2	R64444	hypothetical prote	
24	66	14.4	379	2	F96565	hypothetical prote	
25	66	14.4	415	2	G75179	hypothetical prote	
26	66	14.4	793	2	C83220	hypothetical Prote	
27	66	14.4	983	2	H72510	probable ribonucle	
28	66	14.4	2471	2	T42977	large tegument pro	
29	65.5	14.3	192	2	F72559	hypothetical prote	
							RESULTS
							RESULTS 2
							hypothetical protein MJ1509 - Methanococcus jannaschii
							C;Species: Methanococcus jannaschii
							C;Accession: D64488
							R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Bla
							r, Reich, C.J.; Overbeek, R.; Kirkin, K.G.; Merrick, J.M.; Weinstock, G.F.; Glodek,
							rson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, D.; Roberts, K.M.; Hurst, M.A.
							Science 273, 1058-1073, 1996
							A;Authors: Kaine, B.P.; Borodovsky, M.; Kleink, H.P.; Fraser, C.M.; Smith, H.O.; Woest
							A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
							A;Reference number: A64300; PMID:96337999; PMID:8688087
							A;Accession: D64488
							A;Status: preliminary; nucleic acid sequence not shown; translation not shown
							A;Molecule type: DNA
							A;Residues: 1-153 <BUT>
							A;Cross-references: GB:U67592; GB:L77117; NID:92826425; PIDN:AA899534.1; PID:91500394
							C;Genetics: A;Map position: FOR1482025-1482487
							Query Match Similarity 15.7%; Score 72; DB 2; Length 153;
							Best Local Similarity 28.8%; Pred. No. 3.8;



membrane associated chemotaxis sensory transducer protein (MSP domain and HAMP domain) | A;Molecule type: DNA  
 C;Species: Clostridium acetobutylicum | A;Residues: 1-356 <STO>  
 C;Accession: E97066 | A;Cross-references: GB:NC\_001268; NID:97270398; PIDN:CAB80165.1; GSPDB:GN00140  
 R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koontin, E.V.; Smith, D.R.  
 J.; Bacterium, 183, 482-4838, 2001  
 A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum | A;Position: 4  
 A;Reference number: A96900; MUID:21359325; PMID:21359325; GSPDB:GN00168  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Cross-references: GB:AEO01437; PIDN:AAK79320.1; PID:915024285; GSPDB:GN00168  
 A;Experimental source: Clostridium acetobutylicum ATCC824  
 C;Genetics:  
 A;Gene: CAC1352

Query Match 15.1%; Score 69.5; DB 2; Length 568;  
 Best Local Similarity 24.8%; Pred. No. 27;  
 Matches 27; Conservative 19; Mismatches 44; Indels 19; Gaps 3;  
 Qy 1 MKLVTIFLVTLSCSYATPLINKVPLPVDKL--APLIDNDLPPMDPLKLUKTG 57  
 Db 186 MGILILIISSILSPAATLNNVNIVIKLTVYATSTAENNLADITHNSDELG 245  
 Qy 58 I--SVEHLVEGLRKCYCNELGEAS----EAVKKLLEAL 90  
 Db 246 VLAESFNMSRNLSLINKINTESSNYTDAAYNLQTNTIESSKALEQIA 294

RESULT 8  
 T05269 hypothetical protein T4L20\_50 - Arabidopsis thaliana (Fragment)  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Accession: T05268 | A;Sequence\_revision: 23-Apr-1999 #text\_change 26-Aug-1999  
 R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; Deewes, H.W.; Mayer, K.F.X.; Schieller, C.  
 submitted to the Protein Sequence Database, September 1998  
 A;Reference number: 215406  
 A;Accession: T05268  
 A;Molecule type: DNA  
 A;Cross-references: EMBL:AI023094  
 A;Experimental source: Cultivar Columbia; BAC clone T4L20  
 C;Genetics:  
 A;Map position: 4  
 A;Note: intron positions not resolved  
 C;Superfamily: beta-1,3-glucanase

Query Match 14.9%; Score 68.5; DB 2; Length 335;  
 Best Local Similarity 40.0%; Pred. No. 20;  
 Matches 20; Conservative 10; Mismatches 17; Indels 3; Gaps 2;

Qy 41 NILPFMDPLKLUKTGIGSVEHLVEGLRKCYCNELGEASAEAVKKLLEAL 90  
 Db 80 NVLFYPYPASKMLITVGNEI--LMSNDPNLVNQLLP-AMQNTVRALEAVS 126

RESULT 9  
 D85406 hypothetical protein At4g34480 [imported] - Arabidopsis thaliana  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Accession: D85406 | A;Sequence\_revision: 16-Feb-2001 #text\_change 02-Mar-2001  
 R;anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring Nature 402, 769-771, 1999  
 A;Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
 A;Reference number: A85001; MUID:20083488; PMID:10617198  
 A;Accession: D85406  
 A;Status: preliminary

Query Match 14.9%; Score 68.5; DB 2; Length 356;  
 Best Local Similarity 40.0%; Pred. No. 21;  
 Matches 20; Conservative 10; Mismatches 17; Indels 3; Gaps 2;

Qy 41 NILPFMDPLKLUKTGIGSVEHLVEGLRKCYCNELGEASAEAVKKLLEAL 90  
 Db 101 NVLPYPYPASKMLITVGNEI--LMSNDPNLVNQLLP-AMQNTVRALEAVS 147

RESULT 10  
 T47710 glucuronosyl transferase-like protein - Arabidopsis thaliana  
 N;Alternative names: protein F116\_120  
 C;Species: Arabidopsis thaliana (mouse-ear cress)  
 C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 19-May-2000  
 C;Accession: T47710  
 R;Benes, V.; Wurmbach, B.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lenczke, K.; Mayer, submitted to the Protein Sequence Database, March 2000  
 A;Reference number: Z24473  
 A;Accession: T47710  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-464 <DEN>  
 A;Cross-references: EMBL:AI161667  
 A;Experimental source: cultivar Columbia; BAC clone F116  
 C;Genetics:  
 A;Map position: 3  
 A;Introns: 162/1  
 A;Note: F116\_120  
 C;Superfamily: flavonol 3'-glucosyltransferase

Query Match 14.9%; Score 68.5; DB 2; Length 464;  
 Best Local Similarity 30.6%; Pred. No. 28;  
 Matches 22; Conservative 15; Mismatches 28; Indels 7; Gaps 3;

Qy 13 SLC5SYATAFLINKVPLPVDKLAPLPLDNILPFDMPDKLUKTGIGSVEHLVEGLRKCVN 72  
 Db 142 TFCAYATFPPLLTDKGVLPIQGSR--LDELVTEPLPLIK--VRDLIPVIKTKBPEGNRILN 196

Query Match 14.9%; Score 68.5; DB 2; Length 464;  
 Best Local Similarity 30.6%; Pred. No. 28;  
 Matches 22; Conservative 15; Mismatches 28; Indels 7; Gaps 3;

Qy 73 EL--GPEASBEV 82  
 Db 197 DMVEGAKLSSGV 208

RESULT 11  
 WNVZAI A-type inclusion protein - cowpox virus (strain CP906)  
 C;Species: cowpox virus  
 C;Accession: JQ0006; S01495  
 R;Funahashi, S.; Sato, T.; Shida, H.  
 J. Gen. Virol. 69, 35-47, 1988  
 A;Title: Cloning and characterization of the gene encoding the major protein of the  
 A;Reference number: JQ0006; MUID:88089536; PMID:2826668  
 A;Accession: JQ0006  
 A;Molecule type: DNA  
 A;Residues: 1-1284 <FUN>  
 A;Cross-references: GB:ID00319; NID:9221140; PIDN:BAA00222.1; PMID:9221141  
 R;Patel, D.D.; Pickup, D.J.  
 EMBL J. 6, 3787-3794, 1987  
 A;Title: Messenger RNAs of a strongly-expressed late gene of cowpox virus contain 5'-  
 A;Reference number: S01494; MUID:88111568; PMID:2828037  
 A;Accession: S01495  
 A;Molecule type: DNA  
 A;Residues: 1-109 <PAT>

A;Cross-references: EMBL:X06343  
 C;Superfamily: compx virus A-type inclusion protein  
 C;Keywords: inclusion protein

Query Match 14.9%; Score 68.5; DB 1; Length 1284;  
 Best Local Similarity 36.0%; Pred. No. 82; Gaps 5;  
 Matches 27; Conservative 7; Mismatches 24; Indels 17;

Qy 30 PVDKLAPFLDNL--PFDMP--IKLILKT-LGIS----VHINVEGLKCVNELG--- 75  
 Db 364 PVKVQSKEDDGTPYNNPPEPDYVPTITKVLGIAADYQLVTKLIEWLDKCEEECGGG 423  
 Qy 76 --- PEASAEVKLIE 87  
 Db 424 EYKTELEEAERKRTIE 438

RESULT 12  
 RPBBF5  
 Immunity repressor protein - Bacillus phage phi-105  
 C;Species: Bacillus phage phi-105  
 A;Note: host Bacillus subtilis  
 C;Sequence revision 31-Mar-1988 #text\_change 16-Jun-2000  
 C;Accession: A93579; A91535; S02459; T1354; A24521  
 R;Dbase, P.; Surinck, J.; De Smet, B.; Van Montagu, M.  
 Nucleic Acids Res. 13, 5441-5455, 1985  
 A;Title: Nucleotide sequence and mutational analysis of an immunity repressor gene from  
 A;Reference number: A93579; MUID: 85297750; PMID:2993999  
 A;Molecule type: DNA  
 A;Residues: 1-147 <DNA>  
 A;Cross-references: GB:X02799; NID:915455; PIDN:CAA26567.1; PMID:9579178  
 R;Cully, D.F.; Garro, A.J.  
 Gene 38, 153-164, 1985  
 A;Title: Nucleotide sequence of the immunity region of *Bacillus subtilis* bacteriophage F  
 A;Reference number: A91535; MUID:86056372; PMID:3934047

A;Accession: A91535  
 A;Molecule type: DNA  
 A;Residues: 1-147 <CUL>  
 A;Cross-references: 4-147 <VAN>  
 A;Note: Part of this sequence, including the amino end of the mature protein, was confirmed by submission to the EMBL Data Library, July 1998  
 A;Description: Complete nucleotide sequence of *Bacillus subtilis* phage phi-105.  
 A;Reference number: Z17688  
 A;Accession: T13543  
 A;Status: Preliminary; translated from GB/EMBL/DDJB  
 A;Molecule type: DNA  
 A;Residues: 4-147 <KOB>  
 A;Cross-references: EMBL:AB016282; PIDN:BA35660.1  
 C;Genetics  
 A;Start codon: GTG  
 C;Superfamily: phage phi-105 immunity repressor protein  
 C;Keywords: DNA binding; early protein; repressor; transcription regulation

Query Match 14.8%; Score 68; DB 1; Length 147;  
 Best Local Similarity 24.3%; Pred. No. 9.2; Gaps 2;  
 Matches 25; Conservative 13; Mismatches 33; Indels 32; Gaps 2;

Qy 23 LNKVPLPVDKLAFLDNLIPMDPURLKLTKLGTISVEHIV---- 64  
 Db 24 LAEKANLRSYSLADIERDRYNPSLSLTAVAGALGIVQSATGEETILIKEQAENYSKEE 83

RESULT 13  
 D70359  
 保守 hypothetical protein aq\_674 - Aquifex aeolicus  
 C;Species: Aquifex aeolicus  
 C;Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
 C;Accession: D70359  
 R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.  
 V.; Nature 392, 353-358, 1998  
 A;Title: The complete genome of the hyperthermophilic bacterium *Aquifex aeolicus*.  
 A;Reference number: A70300; MUID:98196666; PMID:9537320  
 A;Accession: D70359  
 A;Status: Preliminary; nucleic acid sequence not shown; translation not shown  
 A;Molecule type: DNA  
 A;Cross-references: 1-239 <AQF>  
 A;Experimental source: strain VF5  
 C;Genetics:  
 A;Gene: aq\_674

Query Match 14.8%; Score 68; DB 2; Length 239;  
 Best Local Similarity 32.6%; Pred. No. 15;  
 Matches 28; Conservative 15; Mismatches 27; Indels 16; Gaps 5;

Qy 9 LVTLVSLC--SYSATTAFLINKVPLPVDKLAFLDNLIPMDPURLKLTKLGTISVEHIVLEG 66  
 Db 160 LYLLSPCPRLYELTSLN-FNLPLRLES-----LYIYPTPLKARLALTIVSKN-VFKG 210

Query Match 14.8%; Score 68; DB 2; Length 236;  
 Best Local Similarity 32.6%; Pred. No. 15;  
 Matches 28; Conservative 15; Mismatches 27; Indels 16; Gaps 5;

Qy 67 LRKC---VNELGPEASRAVKLLE 87  
 Db 211 QLECDKPLLINKGEYTYEVQQLIE 236

RESULT 14  
 C86364  
 hypothetical protein F19G10.4 [imported] - *Arabidopsis thaliana*  
 C;Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C;Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 19-Apr-2002  
 C;Accession: C86364  
 R;Theobald, A.; Becker, J.R.; Palm, C.J.; Federerstiel, N.A.; Kaul, S.; White, O.; Alo Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, Hansen, M.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luos, J.S.; Maiti, R.; Marzi Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Schwartz, P.; Shim, P.; Southwick, A.M.; Sun, H.; Talliker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A;Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A;Reference number: A86141; MUID:21016719; PMID:11130712  
 A;Accession: C86364  
 A;Status: Preliminary  
 A;Molecule type: DNA  
 A;Cross-references: GB:AE005172; NID:92462833; PIDN:AAB72168.1; GSPPDB:GN00141  
 C;Genetics:  
 A;Map position: 1  
 C;Superfamily: ferric reductase FRE2

Query Match 14.8%; Score 68; DB 2; Length 693;  
 Best Local Similarity 31.8%; Pred. No. 48;  
 Matches 34; Conservative 14; Mismatches 37; Indels 22; Gaps 5;

Qy 6 IFLI-VTISLCSYSATAFLINK----VPLPVDKLAFLPPL---DNILIPFMDDPL---- 49  
 Db 584 IYLLSPCPRLYELTSLN-FNLPLRLES-----LYIYPTPLKARLALTIVSKN-VFKG 643

Query Match 14.8%; Score 68; DB 2; Length 693;  
 Best Local Similarity 31.8%; Pred. No. 48;  
 Matches 34; Conservative 14; Mismatches 37; Indels 22; Gaps 5;

Qy 50 ---KULLKGIGSVVHLVGLRKVWNLQPEAS-EAVKMKLRLS 90  
 Db 644 PNLINKLVGLKGSSVGVLCPRKREEVAKICSGFSAAANLQFESSIS 690

Qy 65 -----EGLRKCVNELG-----PEASAEVKLLEALSHV 93  
 Db 84 XDIAKRMEBIRKDLERSDGLSFSPGEPMQSVEAVSLMAMHEHV 126

RESULT 15	
A86238	protein F14N23_31 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)	
C;Accession: A86238	
C;Accession: A86238	#sequence_change 31-Mar-2001
C;Accession: A86238	#sequence_revision 02-Mar-2001
R/Theologians, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, C.; Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Ansens, N.F.; Hughes, B.; Huizar, L.	Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.; C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, Z.A.; Luong, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.	
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.	
A;Title: Sequence and analysis of chromosome 1 of the Plant Arabidopsis.	
A;Reference number: A86141; MUID:21016719; PMID:11130712	
A;Accession: A86238	
A;Status: preliminary	
A;Molecule type: DNA	
A;Residues: 1-512 <STO>	
A;Cross-references: GB:AE005172; NID:94914345; PIDN:AAD32893_1; GSPDB:GN00141	
C;Genetics:	
A;Gene: F14N23_31	
A;Map position: 1	
Query Match Score 67.5; DB 2; Length 512;	
Best Local Similarity 32.8%; Prd. No. 39;	
Matches 19; Conservative 8; Missmatches 16; Indels 15; Gaps 2;	
QY 31 VDKLAPPLDNLPLPMDPLKLKLTGIGSVEVHLLVEGLRKCVNELGGPEASEAVKKLEA 88 380 VEVKVGFLDPTTAPFRERLKIGRVANVDDHL-----SGPE-----KCLMQA 422	



PRIOR FILING DATE: 1997-10-28  
 PRIOR APPLICATION NUMBER: 60/063544  
 / PRIOR FILING DATE: 1997-10-28 File Wrapper or PALM.  
 / NUMBER OF SEQ ID NOS: 612  
 / SEQ ID NO:  
 / LENGTH: 93  
 / TYPE: PRT  
 / ORGANISM: Homo Sapien

US-10-206-915-244

---

Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 MKLVTFILVTLISLCSYATPLINKVPLPVDKLAPLPLDNLPLPKLTKLGIVS 60  
 Db 1 MKLVTFILVTLISLCSYATPLINKVPLPVDKLAPLPLDNLPLPKLTKLGIVS 60

SEQ ID NO: 244  
 LENGTH: 93  
 TYPE: PRT  
 ORGANISM: Homo Sapien

US-10-206-915-244

Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

US-10-201-858-244

RESULT 3

Sequence 244, Application US/10201858  
 Publication No. US20040038337A1  
 GENERAL INFORMATION:  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Chen, Jian  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Pan, James  
 APPLICANT: Smith, Victoria  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

FILE REFERENCE: P1430R1C464

CURRENT APPLICATION NUMBER: US/10/201-858

CURRENT FILING DATE: 2002-07-23

PRIOR APPLICATION NUMBER: 10/052586

PRIOR FILING DATE: 2002-01-15

PRIOR APPLICATION NUMBER: 60/059563

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/059266

PRIOR FILING DATE: 1997-09-18

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/063120

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063121

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063486

PRIOR FILING DATE: 1997-10-21

PRIOR APPLICATION NUMBER: 60/063540

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063541

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063544

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 612

SEQ ID NO 244

LENGTH: 93

TYPE: PRT

ORGANISM: Homo Sapien

US-10-201-858-244

PRIOR FILING DATE: 1997-10-28 File Wrapper or PALM.  
 PRIOR APPLICATION NUMBER: 60/063250  
 PRIOR FILING DATE: 1997-10-17  
 PRIOR APPLICATION NUMBER: 60/063120  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/063121  
 PRIOR FILING DATE: 1997-10-24  
 PRIOR APPLICATION NUMBER: 60/063486  
 PRIOR FILING DATE: 1997-10-21  
 PRIOR APPLICATION NUMBER: 60/063540  
 PRIOR FILING DATE: 1997-10-28  
 PRIOR APPLICATION NUMBER: 60/063541  
 PRIOR FILING DATE: 1997-10-28  
 PRIOR APPLICATION NUMBER: 60/063544  
 PRIOR FILING DATE: 1997-10-28  
 PRIOR APPLICATION data removed - See File Wrapper or PALM.

Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0;  
 Indels 0; Gaps 0;

Qy 1 MKLVTFILVTLISLCSYATPLINKVPLPVDKLAPLPLDNLPLPKLTKLGIVS 60  
 Db 1 MKLVTFILVTLISLCSYATPLINKVPLPVDKLAPLPLDNLPLPKLTKLGIVS 60

SEQ ID NO: 244  
 LENGTH: 93  
 TYPE: PRT  
 ORGANISM: Homo Sapien

US-10-199-670-244

RESULT 4  
US-10-205-890-244  
Sequence 244, Application US/10205890  
Publication No. US20040048334A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanaabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C53B  
CURRENT APPLICATION NUMBER: US/10/208, 024  
CURRENT FILING DATE: 2002-07-29  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 10/052250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/062250  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/059263  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 60/059266  
PRIOR FILING DATE: 1997-09-18  
PRIOR APPLICATION NUMBER: 10/052586  
PRIOR FILING DATE: 2002-01-15  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-17  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063122  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063120  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063121  
PRIOR FILING DATE: 1997-10-24  
PRIOR APPLICATION NUMBER: 60/063486  
PRIOR FILING DATE: 1997-10-21  
PRIOR APPLICATION NUMBER: 60/063540  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063541  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION NUMBER: 60/063544  
PRIOR FILING DATE: 1997-10-28  
PRIOR APPLICATION data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 612  
SEQ ID NO 244  
LENGTH: 93  
TYPE: PRT  
ORGANISM: Homo Sapien  
US-10-208-024-244

Query Match Score 459; DB 12; Length 93;  
Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
Matches 93; Conservate 0; Mismatches 0; Indels 0; Gaps 0;  
RESULT 6  
US-10-201-853-244  
Sequence 244, Application US/10201853  
Publication No. US20040053358A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Gurney, Austin L.  
APPLICANT: Pan, James  
APPLICANT: Smith, Victoria  
APPLICANT: Watanaabe, Colin K.  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME  
FILE REFERENCE: P3430R1C465  
CURRENT APPLICATION NUMBER: US/10/201, 853

RESULT 5  
US-10-208-024-244  
Sequence 244, Application US/10208024  
Publication No. US0040048335A1  
GENERAL INFORMATION:  
APPLICANT: Baker, Kevin P.  
APPLICANT: Chen, Jian  
APPLICANT: Desnoyers, Luc  
APPLICANT: Goddard, Audrey

CURRENT FILING DATE: 2002-07-23  
 / PRIORITY APPLICATION NUMBER: 10/052586  
 / PRIORITY FILING DATE: 2002-01-15  
 / PRIORITY APPLICATION NUMBER: 60/059263  
 / PRIORITY FILING DATE: 1997-09-18  
 / PRIORITY APPLICATION NUMBER: 60/059266  
 / PRIORITY FILING DATE: 1997-09-18  
 / PRIORITY APPLICATION NUMBER: 60/062250  
 / PRIORITY FILING DATE: 1997-10-17  
 / PRIORITY APPLICATION NUMBER: 60/063120  
 / PRIORITY FILING DATE: 1997-10-24  
 / PRIORITY APPLICATION NUMBER: 60/063121  
 / PRIORITY FILING DATE: 1997-10-24  
 / PRIORITY APPLICATION NUMBER: 60/063486  
 / PRIORITY FILING DATE: 1997-10-21  
 / PRIORITY APPLICATION NUMBER: 60/063540  
 / PRIORITY FILING DATE: 1997-10-28  
 / PRIORITY APPLICATION NUMBER: 60/063541  
 / PRIORITY FILING DATE: 1997-10-28  
 / PRIORITY APPLICATION NUMBER: 60/063544  
 / PRIORITY FILING DATE: 1997-10-28  
 / Prior Application data removed - See File Wrapper or PALM.  
 / NUMBER OF SEQ ID NOS: 612  
 / SEQ ID NO:  
 / LENGTH: 93  
 / TYPE: PROTEIN  
 / ORGANISM: Homo Sapien  
 / US-10-201-853-244

Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLVTTIPLVTTISLCSYATAFLINKVLPLVDKLAPELDNTLPFMDKLKLTGKVSV 60  
 Db 1 MKLVTTIPLVTTISLCSYATAFLINKVLPLVDKLAPELDNTLPFMDKLKLTGKVSV 60

Qy 61 EHLVEGLRKCVNELGPSEAAVKLLAHLHLY 93  
 Db 61 EHLVEGLRKCVNELGPSEAAVKLLAHLHLY 93

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RESULT 7  
 / US-10-174-581-244  
 / Sequence 241, Application US-10174581  
 / Publication No. US20030017540A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Baker, Kevin P.  
 / APPLICANT: Chen, Jian  
 / APPLICANT: Destroyers, Luc  
 / APPLICANT: Goddard, Audrey  
 / APPLICANT: Godowski, Paul J.  
 / APPLICANT: Gurney, Austin L.  
 / APPLICANT: Pan, James  
 / APPLICANT: Smith, Victoria  
 / APPLICANT: Watanabe, Colin K.  
 / APPLICANT: Wood, William I.  
 / APPLICANT: Zhang, Zemin  
 / TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 / FILE REFERENCE: P343091C41  
 / CURRENT APPLICATION NUMBER: US/10/174, 581  
 / CURRENT FILING DATE: 2002-06-18  
 / PRIORITY APPLICATION NUMBER: 10/052586  
 / PRIOR FILING DATE: 2002-01-15  
 / PRIORITY APPLICATION NUMBER: 60/059263  
 / PRIOR FILING DATE: 1997-09-18  
 / PRIORITY APPLICATION NUMBER: 60/059266  
 / PRIOR FILING DATE: 1997-09-18  
 / PRIORITY APPLICATION NUMBER: 60/062250  
 / PRIOR FILING DATE: 1997-10-17  
 / PRIORITY APPLICATION NUMBER: 60/063120  
 / PRIOR FILING DATE: 1997-10-24  
 / PRIORITY APPLICATION NUMBER: 60/063486  
 / PRIOR FILING DATE: 1997-10-21  
 / PRIORITY APPLICATION NUMBER: 60/063540  
 / PRIOR FILING DATE: 1997-10-28  
 / PRIORITY APPLICATION NUMBER: 60/063541  
 / PRIOR FILING DATE: 1997-10-28  
 / PRIORITY APPLICATION NUMBER: 60/063544  
 / PRIOR FILING DATE: 1997-10-28  
 / PRIORITY APPLICATION NUMBER: 60/063564  
 / PRIOR FILING DATE: 1997-10-28  
 / PRIORITY APPLICATION NUMBER: 60/063734  
 / PRIOR FILING DATE: 1997-10-29  
 / PRIORITY APPLICATION NUMBER: 60/063870  
 / PRIOR FILING DATE: 1997-10-31  
 / PRIORITY APPLICATION NUMBER: 60/064103  
 / PRIOR FILING DATE: 1997-10-31  
 / PRIORITY APPLICATION NUMBER: 60/065311  
 / PRIOR FILING DATE: 1997-11-13  
 / PRIORITY APPLICATION NUMBER: 60/066120  
 / PRIOR FILING DATE: 1997-11-21  
 / PRIORITY APPLICATION NUMBER: 60/066466  
 / PRIOR FILING DATE: 1997-11-14  
 / PRIORITY APPLICATION NUMBER: 60/066772  
 / PRIOR FILING DATE: 1997-11-24  
 / PRIORITY APPLICATION NUMBER: 60/069335  
 / PRIOR FILING DATE: 1997-12-11  
 / PRIORITY APPLICATION NUMBER: 60/069425  
 / PRIOR FILING DATE: 1997-12-12  
 / PRIORITY APPLICATION NUMBER: 60/069870  
 / PRIOR FILING DATE: 1997-12-17  
 / PRIORITY APPLICATION NUMBER: 60/068017  
 / PRIOR FILING DATE: 1997-12-18  
 / PRIORITY APPLICATION NUMBER: 60/077450  
 / PRIOR FILING DATE: 1998-03-10  
 / PRIORITY APPLICATION NUMBER: 60/077632  
 / PRIOR FILING DATE: 1998-03-11  
 / PRIORITY APPLICATION NUMBER: 60/077649  
 / PRIOR FILING DATE: 1998-03-11  
 / PRIORITY APPLICATION NUMBER: 60/078886  
 / PRIOR FILING DATE: 1998-03-20  
 / PRIORITY APPLICATION NUMBER: 60/078939  
 / PRIOR FILING DATE: 1998-03-27  
 / PRIORITY APPLICATION NUMBER: 60/079786  
 / PRIOR FILING DATE: 1998-03-27  
 / PRIORITY APPLICATION NUMBER: 60/080107  
 / PRIOR FILING DATE: 1998-03-31  
 / PRIORITY APPLICATION NUMBER: 60/080194  
 / PRIOR FILING DATE: 1998-03-31  
 / PRIORITY APPLICATION NUMBER: 60/080327  
 / PRIOR FILING DATE: 1998-04-01  
 / PRIORITY APPLICATION NUMBER: 60/080333  
 / PRIOR FILING DATE: 1998-04-01  
 / PRIORITY APPLICATION NUMBER: 60/081049  
 / PRIOR FILING DATE: 1998-04-08  
 / PRIORITY APPLICATION NUMBER: 60/081070  
 / PRIOR FILING DATE: 1998-04-08  
 / PRIORITY APPLICATION NUMBER: 60/081195  
 / PRIOR FILING DATE: 1998-04-09  
 / PRIORITY APPLICATION NUMBER: 60/081838  
 / PRIOR FILING DATE: 1998-04-15  
 / PRIORITY APPLICATION NUMBER: 60/082568  
 / PRIOR FILING DATE: 1998-04-21  
 / PRIORITY APPLICATION NUMBER: 60/082569  
 / PRIOR FILING DATE: 1998-04-21  
 / PRIORITY APPLICATION NUMBER: 60/082704  
 / PRIOR FILING DATE: 1998-04-22  
 / PRIORITY APPLICATION NUMBER: 60/082797  
 / PRIOR FILING DATE: 1998-04-22  
 / PRIORITY APPLICATION NUMBER: 60/083322  
 / PRIOR FILING NUMBER: 60/083322

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; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088B25
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088867
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

Query Match          100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Indels 0; Gaps 0;

; MKLVTIFLLTVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPMDPLKLLKLTKLGIVY 60
Qy   1 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   1 ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

; MKLVTIFLLTVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPMDPLKLLKLTKLGIVY 60
Qy   61 EHLVEGLRKCYNELGPEASEAVKKVLEALSHLV 93
Db   61 EHLVEGLRKCYNELGPEASEAVKKVLEALSHLV 93

RESULT 8
US-10-176-483-244
; Sequence 244, Application US/10176483
; Publication No. US20030017541A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; ACIDS ENCODING THE SAME
FILE REFERENCE: P3430RLC68
CURRENT APPLICATION NUMBER: US/10/176,483
CURRENT FILING DATE: 2002-06-20
Prior application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 612
SEQ ID NO 244
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-483-244

Query Match          100.0%; Score 459; DB 12; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 93; Conservative 0; Indels 0; Gaps 0;
Qy   1 MKLVTIFLLTVTISLCSYSATAFLINKVPLPVDKLAPLPLDNILPMDPLKLLKLTKLGIVY 60

```

Db 1 MKLVTFLLVITISLCSYSATAFLINKVPLPVDKLAPLDNLPPMDPLKLLKLTLGIVS 60  
 Qy 61 EHLVEGLRKCVNELGPBASEAVKKLLEALSHLV 93  
 Db 61 EHLVEGLRKCVNELGPBASEAVKKLLEALSHLV 93

## RESULT 9

US-10-176-749-244

; Sequence 244, Application US/10176749

; Publication No. US20030017542A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zemin, Zhang

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; ACIDS ENCODING THE SAME

; FILE REFERENCE: P3410R1C76

; CURRENT APPLICATION NUMBER: US/10/176,749

; CURRENT FILING DATE: 2002-06-20

; PRIOR APPLICATION removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO: 244

; LENGTH: 93

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-176-749-244

Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLVTFLLVITISLCSYSATAFLINKVPLPVDKLAPLDNLPPMDPLKLLKLTLGIVS 60

Db 1 EHLVEGLRKCVNELGPBASEAVKKLLEALSHLV 93

Db 61 EHLVEGLRKCVNELGPBASEAVKKLLEALSHLV 93

## RESULT 10

US-10-176-914-244

; Sequence 244, Application US/10176914

; Publication No. US20030017543A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zemin, Zhang

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; ACIDS ENCODING THE SAME

; FILE REFERENCE: P3420R1C83

; CURRENT APPLICATION NUMBER: US/10/176,914

; CURRENT FILING DATE: 2002-06-20

; PRIOR APPLICATION removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLVTFLLVITISLCSYSATAFLINKVPLPVDKLAPLDNLPPMDPLKLLKLTLGIVS 60

Db 1 EHLVEGLRKCVNELGPBASEAVKKLLEALSHLV 93

Db 61 EHLVEGLRKCVNELGPBASEAVKKLLEALSHLV 93

;

## RESULT 11

US-10-176-915-244

; Sequence 244, Application US/10176915

; Publication No. US20030017544A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zemin, Zhang

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C10

; CURRENT APPLICATION NUMBER: US/10/176,915

; CURRENT FILING DATE: 2002-06-21

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO: 244

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-176-915-244

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C11

; CURRENT APPLICATION NUMBER: US/10/176,915

; CURRENT FILING DATE: 2002-06-21

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO: 244

; TYPE: PRT

; ORGANISM: Homo Sapien

; US-10-176-915-244

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C12

; CURRENT APPLICATION NUMBER: US/10/176,915

; CURRENT FILING DATE: 2002-06-21

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

RESULT 13  
 US-10-180-550-244  
 ; Sequence 244, Application US/10180550  
 ; Publication No. US2003006440A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430RIC149  
 ; CURRENT APPLICATION NUMBER: US/10/180, 550  
 ; CURRENT FILING DATE: 2002-05-25  
 ; Prior application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO: 244  
 ; LENGTH: 93  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-176-484-244  
 Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MKLVTTFLVTTISLCSYSATFLINKVPLPVDKAPLPLDNILPFMDPLKLLKLGIVS 60  
 Db 1 MKLVTTFLVTTISLCSYSATFLINKVPLPVDKAPLPLDNILPFMDPLKLLKLGIVS 60  
 Qy 61 EHLVEGIRKCVCNELGPEASEAVKKLEALSHLV 93  
 Db 61 EHLVEGIRKCVCNELGPEASEAVKKLEALSHLV 93  
 RESULT 14  
 US-10-180-550-244  
 ; Sequence 244, Application US/10180550  
 ; Publication No. US2003006440A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Baker, Kevin P.  
 ; APPLICANT: Chen, Jian  
 ; APPLICANT: Desnoyers, Luc  
 ; APPLICANT: Goddard, Audrey  
 ; APPLICANT: Godowski, Paul J.  
 ; APPLICANT: Gurney, Austin L.  
 ; APPLICANT: Pan, James  
 ; APPLICANT: Smith, Victoria  
 ; APPLICANT: Watanabe, Colin K.  
 ; APPLICANT: Wood, William I.  
 ; APPLICANT: Zhang, Zemin  
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
 ; ACIDS ENCODING THE SAME  
 ; FILE REFERENCE: P3430RIC149  
 ; CURRENT APPLICATION NUMBER: US/10/180, 550  
 ; CURRENT FILING DATE: 2002-05-25  
 ; Prior application removed - See File Wrapper or Palm  
 ; NUMBER OF SEQ ID NOS: 612  
 ; SEQ ID NO: 244  
 ; LENGTH: 93  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapien  
 ; US-10-180-550-244  
 Query Match 100.0%; Score 459; DB 12; Length 93;  
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;  
 Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 MKLVTTFLVTTISLCSYSATFLINKVPLPVDKAPLPLDNILPFMDPLKLLKLGIVS 60  
 Db 1 MKLVTTFLVTTISLCSYSATFLINKVPLPVDKAPLPLDNILPFMDPLKLLKLGIVS 60  
 Qy 61 EHLVEGIRKCVCNELGPEASEAVKKLEALSHLV 93  
 Db 61 EHLVEGIRKCVCNELGPEASEAVKKLEALSHLV 93  
 RESULT 14

Qy	1	MKLQTIFLVITISLCSYSATAPLLINKVPLVDKLAALPLDNILPFLMDPKLKKLKGISV 60
Db	1	MKLQTIFLVITISLCSYSATAPLLINKVPLVDKLAALPLDNILPFLMDPKLKKLKGISV 60
Qy	61	EHLVEGLRKCYNEIGPGEASEAVKKLLEALSHV 93
Db	61	RHVEGLRKCYNNGPGEASEAVKKLLEALSHV 93

Search completed: June 2, 2004, 20:25:18  
Job time : 17.5802 secs

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Gencore version 5.1.6

OM protein - protein search, using sw model

Run on: June 2, 2004, 20:16:40 ; Search time 6.48136 seconds  
 (without alignments)  
 740.773 Million cell updates/sec

Title: US-09-700-770-7

Perfect score: 459

Sequence: 1 MKLVTFLLVTRISCSAT.....LGPEASEAVKXKLEALSHLV 93

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*

- 1: /cgn2\_6/pcodata/2/iaa/5A\_COMB.pep:\*
- 2: /cgn2\_6/pcodata/2/iaa/5B\_COMB.pep:\*
- 3: /cgn2\_6/pcodata/2/iaa/6A\_COMB.pep:\*
- 4: /cgn2\_6/pcodata/2/iaa/6B\_COMB.pep:\*
- 5: /cgn2\_6/pcodata/2/iaa/PCTO2\_COMB.pep:\*
- 6: /cgn2\_6/pcodata/2/iaa/backfiles.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No. Score

Query Match Length

DB ID

Description

Result No.

Score

Query

Match

Length

DB ID

Description

1	459	100.0	93	2	US-09-984-725-14	Sequence 14, Appl
2	84	18.3	17	2	US-09-964-725-15	Sequence 15, Appl
3	77	16.8	15	2	US-09-964-725-18	Sequence 18, Appl
4	77	16.8	18	2	US-09-964-725-19	Sequence 19, Appl
5	76	16.6	17	2	US-09-964-725-17	Sequence 17, Appl
6	75.5	16.4	90	3	US-09-821-451A-4	Sequence 4, Appl
7	75.5	16.4	90	3	US-09-265-810-4	Sequence 4, Appl
8	75.5	16.4	90	3	US-09-914-276-15	Sequence 15, Appl
9	75.5	16.4	90	4	US-09-583-169-4	Sequence 4, Appl
10	75.5	16.4	90	4	US-09-215-918-6	Sequence 6, Appl
11	75.5	16.4	90	4	US-09-467-602A-6	Sequence 6, Appl
12	73	15.9	446	4	US-09-134-000C-343A-4	Sequence 27, Appl
13	69	15.0	95	3	US-09-821-451A-27	Sequence 27, Appl
14	69	15.0	95	3	US-09-263-810-27	Sequence 7, Appl
15	69	15.0	95	4	US-09-583-169-27	Sequence 7, Appl
16	67.5	14.7	421	4	US-09-328-352-714A	Sequence 7, Appl
17	67	14.6	95	1	US-09-455-896-7	Sequence 7, Appl
18	67	14.6	95	2	US-09-933-149-7	Sequence 7, Appl
19	67	14.6	95	2	US-09-082-343-7	Sequence 7, Appl
20	67	14.6	95	3	US-09-082-253-7	Sequence 7, Appl
21	67	14.6	95	4	US-09-162-622-7	Sequence 7, Appl
22	67	14.6	95	4	US-09-0509-015-7	Sequence 7, Appl
23	67	14.6	95	5	PCT-US96-08235-7	Sequence 7, Appl
24	66.5	14.5	91	1	US-09-493-149-8	Sequence 8, Appl
25	66.5	14.5	91	2	US-09-082-343-8	Sequence 8, Appl
26	66.5	14.5	91	3	US-09-082-253-8	Sequence 8, Appl

## ALIGNMENTS

RESULT 1  
 US-09-964-725-14

; Sequence 14, Application US/08964725  
 ; Patent No. 5939265

; GENERAL INFORMATION:

; / APPLICANT: COHEN, Maurice  
 ; / APPLICANT: FRIDMAN, Paula N.  
 ; / APPLICANT: GORDON, Julian  
 ; / APPLICANT: HODGES, Steven C.  
 ; / APPLICANT: KLAAS, Michael R.  
 ; / APPLICANT: KRATOCHVIL, Jon D.  
 ; / APPLICANT: ROBERTS-RAPP, Lisa  
 ; / APPLICANT: ROSELLI, John C.  
 ; / APPLICANT: STROUPE, Steven D.  
 ; / TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
 ; / FOR DETECTING DISEASES OF THE LUNG  
 ; / NUMBER OF SEQUENCES: 19  
 ; / CORRESPONDENCE ADDRESS:  
 ; / ADDRESSEE: Abbott Laboratories  
 ; / STREET: 100 Abbott Park Road  
 ; / CITY: Abbott Park  
 ; / STATE: IL  
 ; / COUNTRY: USA  
 ; / ZIP: 60064-3500  
 ; / COMPUTER READABLE FORM:  
 ; / MEDIUM TYPE: Diskette  
 ; / COMPUTER: IBM Compatible  
 ; / OPERATING SYSTEM: DOS  
 ; / SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; / CURRENT APPLICATION DATA:  
 ; / APPLICATION NUMBER: US/08/964,725  
 ; / FILING DATE:  
 ; / CLASSIFICATION: 435  
 ; / PRIOR APPLICATION DATA:  
 ; / APPLICATION NUMBER:  
 ; / FILING DATE:  
 ; / ATTORNEY/AGENT INFORMATION:  
 ; / NAME: Becker, Cheryl L.  
 ; / REGISTRATION NUMBER: 31,441  
 ; / REFERENCE/DOCKET NUMBER: 5997.US.P1  
 ; / TELECOMMUNICATION INFORMATION:  
 ; / TELEPHONE: 847/938-2623  
 ; / FAX:  
 ; / INFORMATION FOR SEQ ID NO: 14:  
 ; / SEQUENCE CHARACTERISTICS:  
 ; / LENGTH: 93 amino acids  
 ; / TYPE: amino acid  
 ; / STRANDEDNESS: single  
 ; / TOPOLOGY: linear

```

MOLECULE TYPE: No. 5939265E
US - 08-964-725-14

Query Match 100.0%; Score 459; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 2.8e-47;
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          1 MKLVTTFLVITISLCSYSATAFLINKVPLPVDKAPLPLDNILPPMDPKLKLKLGISV 60
Ddb          1 MKLVTTFLVITISLCSYSATAFLINKVPLPVDKAPLPLDNILPPMDPKLKLKLGISV 60
          61 EHLVEGLRKVCNNELGPEASAVKVLLEALSHLV 93
          61 EHLVEGLRKVCNNELGPEASAVKVLLEALSHLV 93

QY          1 MKLVTTFLVITISLCSYSATAFLINKVPLPVDKAPLPLDNILPPMDPKLKLKLGISV 60
Ddb          1 MKLVTTFLVITISLCSYSATAFLINKVPLPVDKAPLPLDNILPPMDPKLKLKLGISV 60
          61 EHLVEGLRKVCNNELGPEASAVKVLLEALSHLV 93
          61 EHLVEGLRKVCNNELGPEASAVKVLLEALSHLV 93

RESULT 2
Sequence 15, Application US/08964725
Patent No. 5939265
GENERAL INFORMATION:
APPLICANT: COHEN, Maurice
APPLICANT: FRIEDMAN, Paula N.
APPLICANT: GORDON, Julian
APPLICANT: HODGES, Steven C.
APPLICANT: KLAFF, Michael R.
APPLICANT: KRAITCHKIL, Jon D.
APPLICANT: ROBERTS-RAPP, Lisa
APPLICANT: RUSSELL, John C.
APPLICANT: SIROUPE, Steven D.
TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE LUNG
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Abbott Laboratories
STREET: 100 Abbott Park Road
CITY: Abbott Park
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PAT-SEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/964,725
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Becker, Chery L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5997.US.P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847/935-1729
TELEFAX: 847/938-2623
TELEX:
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5939265E
US - 08-964-725-15

Query Match 18.3%; Score 84; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

RESULT 3
US-08-964-725-18
; Sequence 18, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
; APPLICANT: FRIEDMAN, Paula N.
; APPLICANT: GORDON, Julian
; APPLICANT: HODGES, Steven C.
; APPLICANT: KLASA, Michael R.
; APPLICANT: KRATOCHVIL, Jon D.
; APPLICANT: ROBERTS-RAPP, Lisa
; APPLICANT: RUSSELL, John C.
; APPLICANT: STRUPEK, Steven D.
; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL
; FOR DETECTING DISEASES OF THE LUNG
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Abbott Laboratories
; STREET: 100 Abbott Park Road
; CITY: Abbott Park
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; FILING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/964,725
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Becker, Cherry L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5997.US.P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847/935-1729
; TELEFAX: 847/938-2623
; TELEX:
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: No. 5939265E
; US-08-964-725-18

Query Match 16.8%; Score 77; DB 2; Length 1
Best Local Similarity 100.0%; Pred. No. 0.0072;
Matches 15; Conservative 0; Mismatches 0; Indel 0
QY 67 LRKCYNTELGPGEASEA 81
Db 1 LRKCYNTELGPGEASEA 15

RESULT 4
US-08-964-725-19
; Sequence 19, Application US/08964725
; Patent No. 5939265
; GENERAL INFORMATION:
; APPLICANT: COHEN, Maurice
;
```

APPLICANT: FRIEDMAN, Paula N.  
 APPLICANT: GORDON, Julian C.  
 APPLICANT: HODGES, Steven C.  
 APPLICANT: KLAAS, Michael R.  
 APPLICANT: KRATOVIL, Jon D.  
 APPLICANT: ROBERTS-RAPP, Lisa  
 APPLICANT: RUSSELL, John C.  
 APPLICANT: STROPE, Steven D.  
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE LUNG  
 NUMBER OF SEQUENCES: 19  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/964,725  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Becker, Cheryl L.  
 REGISTRATION NUMBER: 35,441  
 REFERENCE/DOCKET NUMBER: 5997.US.P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847/935-1729  
 TELEFAX: 847/938-2623  
 TELEX:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Becker, Cheryl L.  
 REGISTRATION NUMBER: 35,441  
 REFERENCE/DOCKET NUMBER: 5997.US.P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847/935-1729  
 TELEFAX: 847/938-2623  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 19:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 18 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 5939265e  
 US-08-964-725-19

RESULT 5  
 Query Match 16.8%; Score 77; DB 2; Length 18;  
 Best Local Similarity 100.0%; Pred. No. 0.0091; Indels 0; Gaps 0;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 77 EASEAVKGGLEALSHLV 93  
 Db 1 EASEAVKGGLEALSHLV 17

US-08-964-725-17  
 Sequence 17, Application US/08964725  
 Patent No. 5939265  
 GENERAL INFORMATION:  
 APPLICANT: COHEN, Maurice N.  
 APPLICANT: FRIEDMAN, Paula N.  
 APPLICANT: GORDON, Julian C.  
 APPLICANT: HODGES, Steven C.  
 APPLICANT: KLAAS, Michael R.  
 APPLICANT: KRATOVIL, Jon D.  
 APPLICANT: ROBERTS-RAPP, Lisa  
 APPLICANT: RUSSELL, John C.  
 APPLICANT: STROPE, Steven D.  
 TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR DETECTING DISEASES OF THE LUNG  
 NUMBER OF SEQUENCES: 19

CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Abbott Laboratories  
 STREET: 100 Abbott Park Road  
 CITY: Abbott Park  
 STATE: IL  
 COUNTRY: USA  
 ZIP: 60064-3500  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Diskette  
 COMPUTER: IBM Compatible  
 OPERATING SYSTEM: DOS  
 SOFTWARE: FASTSEQ for Windows Version 2.0  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/964,725  
 FILING DATE:  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER:  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Becker, Cheryl L.  
 REGISTRATION NUMBER: 35,441  
 REFERENCE/DOCKET NUMBER: 5997.US.P1  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 847/935-1729  
 TELEFAX: 847/938-2623  
 TELEX:  
 INFORMATION FOR SEQ ID NO: 17:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 17 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: No. 5939265e  
 US-08-964-725-17

Query Match 16.6%; Score 76; DB 2; Length 17;  
 Best Local Similarity 100.0%; Pred. No. 0.011; Indels 0; Gaps 0;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 LLKTIGISVEHLYVGL 67  
 Db 1 LLKTIGISVEHLYVGL 16

RESULT 6  
 US-08-811-451A-4  
 Sequence 4, Application US/08821451A  
 Patent No. 6066724  
 GENERAL INFORMATION:  
 APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
 TITLE OF INVENTION: Human Endometrial Specific Steroid  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ADDRESS: CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/821,451A  
 FILING DATE: March 21, 1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 60/014,724

FILING DATE: March 21, 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-821-451A-4

Query Match 16.4%; Score 75 5; DB 3; Length 90;  
Best Local Similarity 27.0%; Pred. No. 0.11; Mismatches 18; Indels 34; Gaps 5;  
Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

Qy 1 MKLVTFILVLTISCSYATFLINKVLPVVDKLAPLPLDNILPFM---DPL-KLLKTL 56  
Db 1 MKLVCFILVLTISCSYATFLINKVLPVVDKLAPLPLDNILPFM---DPL-KLLKTL 49

Qy 57 GISVEHLVE- GLRKCYNELGPE---ASRAVKKLLAEALS 90  
Db 50 DAPPEAAAKLGVRCTDQMSLQRSLIAEVLKTKCS 89

RESULT 7  
US-09-263-810-4  
Sequence 4, Application US/09263810  
Patient No. 617492

GENERAL INFORMATION:  
APPLICANT: Jian-Ni, Guo-Liang Yu and Reiner Gentz  
TITLE OF INVENTION: Human Endometrial Specific Steroid-Binding Factor I, II and III  
TITLE OF INVENTION: Binding Factor I, II and III  
NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07668

COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
APPLICATION NUMBER: US/09/263,810  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/821,451  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: MULLINS, J.G.  
REGISTRATION NUMBER: 33,073  
REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS: LINEAR  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN

RESULT 8  
US-08-912-276-15  
Sequence 15, Application US/08912276  
Patient No. 6183952

GENERAL INFORMATION:  
APPLICANT: Billing-Meddel, Patricia A.  
APPLICANT: Cohen, Maurice  
APPLICANT: Colpitts, Tracey L.  
APPLICANT: Friedman, Paula N.  
APPLICANT: Gordon, Julian  
APPLICANT: Granados, Edward N.  
APPLICANT: Hodges, Steven C.  
APPLICANT: Klass, Michael R.  
APPLICANT: Kratochvil, Jon D.  
APPLICANT: Roberts-Rapp, Lisa  
APPLICANT: Russell, John C.  
APPLICANT: Stroupe, Steven D.

TITLE OF INVENTION: REAGENTS AND METHODS USEFUL  
FOR DETECTING DISEASES OF THE BREAST

NUMBER OF SEQUENCES: 25

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Abbott Laboratories  
STREET: 100 Abbott Park Road  
CITY: Abbott Park  
STATE: IL  
COUNTRY: USA  
ZIP: 60064-3500

COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSQL FOR Windows Version 2.0

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/912,276  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/821,451  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Becker, Cheryl L.  
REGISTRATION NUMBER: 35,441  
REFERENCE/DOCKET NUMBER: 5972-US-P1  
TELEPHONE: 847/935-1729  
TELEFAX: 847/938-2623  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 90 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: No. 6183952e

US-08-912-276-15

Query Match 16.4%; Score 75 5; DB 3; Length 90;  
Best Local Similarity 27.0%; Pred. No. 0.11;

Matches 27; Conservative 18; Mismatches 34; Indels 21; Gaps 5;

GENERAL INFORMATION:  
 ; APPLICANT: Colpitts, Tracey  
 ; TITLE OF INVENTION: REAGENTS AND METHODS USEFUL FOR  
 ; DETECTING DISEASES OF THE BREAST  
 ; FILE REFERENCE: 5972-US-P2  
 ; CURRENT APPLICATION NUMBER: US/09/215,818A  
 ; CURRENT FILING DATE: 1998-12-18  
 ; EARLIER APPLICATION NUMBER: US/912,276  
 ; EARLIER FILING DATE: 1997-08-17  
 ; EARLIER APPLICATION NUMBER: US/09/215,818A  
 ; EARLIER FILING DATE: 1996-08-19  
 ; EARLIER APPLICATION NUMBER: US/09/215,818A  
 ; EARLIER FILING DATE: 1997-08-15  
 ; EARLIER APPLICATION NUMBER: US/09/215,818A  
 ; EARLIER FILING DATE: 1996-08-19  
 ; NUMBER OF SEQ ID NOS: 6  
 ; SOFTWARE: FastSEQ for Windows Version 3.0  
 ; SEQ ID NO: 6  
 ; LENGTH: 90  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens  
 ; US-09-215-818-6

Query Match 16.4%; Score 75.5; DB 4; Length 90;  
 Best Local Similarity 27.0%; Pred. No. 0.11; Mismatches 18; Indels 21; Gaps 5;

QY 1 MKLVVFLVLTISLCSYSSATAFLINKVPLPVDKLAPLPLDNLIPFM--DPL-KLLIKTL 56  
 1 MKLSVCLLVLTLALCCYQANA-----EFCPALVSELLDFFSEPLFKSLAKF 49

Db 57 GISVEHLV--GLRKCVNELGPE---ASEAVKKILEALS 90

QY 50 DAPPEAAAKLGVRKCTDQMSLQRSLIAEVLYKILKCS 89

RESULT 9  
 US-09-583-169-4  
 ; Sequence 4, Application US/09583169  
 ; Patent No. 6338948  
 GENERAL INFORMATION:  
 ; APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
 ; TITLE OF INVENTION: Human Endometrial Specific Steroid-TITLE OF INVENTION: Binding Factor I, II and III  
 ; NUMBER OF SEQUENCES: 27  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ; STREET: 6 BECKER, STEWART & OLSTEIN  
 ; CITY: ROSELAND  
 ; STATE: NEW JERSEY  
 ; COUNTRY: USA  
 ; ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 TELECOMMUNICATION INFORMATION:  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/583,169  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/821,451  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MULLINS, J.G.  
 REGISTRATION NUMBER: 33 073  
 REFERENCE/DOCKET NUMBER: 325800-521 (PP257)  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 4 :  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 90 AMINO ACIDS  
 TYPE: AMINO ACID  
 STRANDEDNESS:  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: PROTEIN  
 US-09-583-169-4

Query Match 16.4%; Score 75.5; DB 4; Length 90;  
 Best Local Similarity 27.0%; Pred. No. 0.11; Mismatches 18; Indels 21; Gaps 5;

QY 1 MKLVVFLVLTISLCSYSSATAFLINKVPLPVDKLAPLPLDNLIPFM--DPL-KLLIKTL 56  
 1 MKLSVCLLVLTLALCCYQANA-----EFCPALVSELLDFFSEPLFKSLAKF 49

Db 57 GISVEHLV--GLRKCVNELGPE---ASEAVKKILEALS 90

QY 50 DAPPEAAAKLGVRKCTDQMSLQRSLIAEVLYKILKCS 89

RESULT 10  
 US-09-215-818-6  
 ; Sequence 6, Application US/09215818A  
 ; Patent No. 6379671

Query Match 16.4%; Score 75.5; DB 4; Length 90;  
 Best Local Similarity 27.0%; Pred. No. 0.11; Mismatches 18; Indels 21; Gaps 5;

QY 1 MKLVVFLVLTISLCSYSSATAFLINKVPLPVDKLAPLPLDNLIPFM--DPL-KLLIKTL 56  
 1 MKLSVCLLVLTLALCCYQANA-----EFCPALVSELLDFFSEPLFKSLAKF 49

Db 1 MKLSVCLLVLTLALCCYQANA-----EFCPAVLSELLDFFFSEPLFKLSLAKF 49  
 Qy 57 GIVEHILVE--GIRKCVNELGP-----ASEAVKRLLEALS 90  
 Db 50 DAPPEAAVAKLGIVKRCTDQMSLQKRSLIAEVLKILKCS 89

RESULT 12  
 US-09-134-000C-3434  
 Sequence 3434, Application US/09134000C  
 Patent No. 6617156  
 GENERAL INFORMATION:  
 APPLICANT: Lynn Doucette-Stamm et al  
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO  
 TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS  
 FILE REFERENCE: 032196-032  
 CURRENT APPLICATION NUMBER: US/09/134,000C  
 CURRENT FILING DATE: 1998-08-13  
 PRIOR APPLICATION NUMBER: US 60/055,778  
 PRIOR FILING DATE: 1997-08-15  
 NUMBER OF SEQ ID NOS: 6812  
 SOFTWARE: Patentin version 3.1  
 SEQ ID NO: 3434  
 LENGTH: 446  
 TYPE: PRT  
 ORGANISM: Enterococcus faecalis  
 US-09-134-000C-3434

Query Match 15.9%; Score 73; DB 4; Length 446;  
 Best Local Similarity 26.3%; Pred. No. 1.8; Gaps 5;  
 Matches 26; Conservative 29; Mismatches 34; Indels 10; Gaps 5;

Qy 4 VTIIFLVITISIC--SYSATAP-LINKY--PLPVDFKLAPLPLDNILPFMDPILKL--LIXTL 56  
 Db 308 VTIILYVQVSESEQFPSTVLTIBLTFEDLSLVPASLVTFLIPVFFLFGYIKSI 367

Qy 57 GISVE--HLVYGLRKCNELGEASEAVKRLLEALSH 92  
 Do 368 GVGGLNLHDMSMRFKELQVSESEKSLSKOLANDL 406

RESULT 13  
 US-08-821-451A-27  
 Sequence 27, Application US/08821451A  
 Patient No. 6066724  
 GENERAL INFORMATION:  
 APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
 TITLE OF INVENTION: Human Endometrial Specific Steroid-  
 TITLE OF INVENTION: Binding Factor I, II and III  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ADDRESS: CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068

COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/263,810  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/821,451  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MULLINS, J.G.  
 REGISTRATION NUMBER: 33,073  
 REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 95 AMINO ACIDS  
 TYPE: AMINO ACID  
 STRANDEDNESS: SINGLE  
 TOPOLogy: LINEAR  
 MOLECULE TYPE: PROTEIN

US-09-263-810-27

Query Match 15.0%; Score 69; DB 3; Length 95;  
 Best Local Similarity 27.5%; Pred. No. 0.71;

Matches 25; Conservative 21; Mismatches 37; Indels 8; Gaps 3;  
 Patent No. 6,38948  
 Sequence 27, Application US/09583169

GENERAL INFORMATION:  
 APPLICANT: Jian Ni, Guo-Liang Yu and Reiner Gentz  
 TITLE OF INVENTION: Human Endometrial Specific Steroid-TITLE OF INVENTION: Binding Factor I, II and III  
 NUMBER OF SEQUENCES: 27  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
 ADDRESS: CECCHI, STEWART & OLSTEIN  
 STREET: 6 BECKER FARM ROAD  
 CITY: ROSELAND  
 STATE: NEW JERSEY  
 COUNTRY: USA  
 ZIP: 07068  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 3.5 INCH DISKETTE  
 COMPUTER: IBM PS/2  
 OPERATING SYSTEM: MS-DOS  
 SOFTWARE: WORD PERFECT 5.1  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/583,169  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/921,451  
 FILING DATE:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MULLINS, J. G.  
 REGISTRATION NUMBER: 33,073  
 REFERENCE/DOCKET NUMBER: 325800-521 (PF257)  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 201-994-1700  
 TELEFAX: 201-994-1744  
 INFORMATION FOR SEQ ID NO: 27:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 95 AMINO ACIDS  
 TYPE: AMINO ACID  
 STRANDEDNESS: SINGLE  
 TOPOLOGY: LINEAR  
 MOLECULE TYPE: PROTEIN  
 US-09-583-169-27

RESULT 15  
 US-09-583-169-27  
 Sequence 27, Application US/09583169  
 1 MKLVTLFLVTTISLCSY-SATAFLINKVPLPVDKAPLPLDNLILPFDPLKLUKTGTS 59  
 1 MKLVTLFLVTTIPICCYASGGCSI-----LDEVTRGTNSTVTLHDYMKLVKPYQAH 54  
 QY 60 -VEHLVEGRKRCVNELGPEASEAVKLLAL 89  
 Db 55 FTERAKVQFKQCFLDQDTKTLENVGYMMEAI 85

Query Match 15.0%; Score 69; DB 4; Length 95;  
 Best Local Similarity 27.5%; Pred. No. 0.71; Matches 21; Mismatches 37; Indels 8; Gaps 3;  
 Matches 25; Conservative 21; Mismatches 37; Indels 8; Gaps 3;

QY 1 MKLVTLFLVTTISLCSY-SATAFLINKVPLPVDKAPLPLDNLILPFDPLKLUKTGTS 59  
 Db 1 MKLVTLFLVTTIPICCYASGGCSI-----LDEVTRGTNSTVTLHDYMKLVKPYQAH 54

QY 60 -VEHLVEGRKRCVNELGPEASEAVKLLAL 89  
 Db 55 FTERAKVQFKQCFLDQDTKTLENVGYMMEAI 85

Search completed: June 2, 2004, 20:23:15  
 Job time : 7.48136 secs

Result No.	Query	Score	Match	Length	DB ID	Description
1	AAGW2068	93	2	AAW2068	Aaw62068 Human lun	
2	AAV28334	93	2	AAV28334	Aay28334 LU103 spe	
3	AAY44456	93	3	AAY44456	Aay44456 Human lun	
4	AAV7289	93	3	AAV7289	Aay87289 Human sig	
5	AATU9145	93	4	AATU9145	Aau29145 Human PRO	
6	ABU88069	93	6	ABU88069	Abi88069 Novel hum	
7	ABU88069	93	6	ABU88069	Abi88069 Novel hum	
8	ABU88384	93	6	ABU88384	Abi88384 Human sec	
9	ABR66258	93	6	ABR66258	Abi66258 Human sec	
10	ABU9588	93	6	ABU9588	Abi9588 Human sec	
11	ABU82827	93	6	ABU82827	Abi82827 Human PRO	
12	ABU9948	93	6	ABU9948	Abi9948 Novel hum	
13	ABU88948	93	6	ABU88948	Abi88948 Human sec	
14	ABR6197	93	6	ABR6197	Abi6197 Human ute	
15	AAO13894	93	6	AAO13894	Abi96250 Novel hum	
16	ABU96250	93	6	ABU96250	Abi92681 Human sec	
17	ABO08758	93	6	ABO08758	Abi08758 Human sec	
18	ABO02810	93	6	ABO02810	Abi02810 Human sec	
19	ABR74964	93	6	ABR74964	Abi74964 Human sec	
20	ABR64726	93	6	ABR64726	Abi64726 Human sec	
21	ABU85599	93	6	ABU85599	Abi85699 Human PRO	
22	ABU98859	93	6	ABU98859	Abi98859 Novel hum	
23	ABU98074	93	6	ABU98074	Abi98074 Novel hum	
24	ABU91780	93	6	ABU91780	Abi91780 Novel hum	

				61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93
Query Match	100.0% ; Score 459; DB 2; Length 93;			
Best Local Similarity	100.0% ; Pred. No. 5.6e-47;			
Matches	93 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;			
		RESULT 3		
Qy	1 MKLVTIFLLTVTISCSYATAFLINKVLPVYDKLAPLPLDNILPFMDPKLKLTKLIGISV 60			
Db	1 MKLVTIFLLTVTISCSYATAFLINKVLPVYDKLAPLPLDNILPFMDPKLKLTKLIGISV 60			
		XX		
Qy	61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93			
Db	61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93			
		XX		
		RESULT 2		
Qy	AY28334 standard; protein; 93 AA.			
Db	AY28334 standard; protein; 93 AA.			
		XX		
AC	AY28334;			
XX	19-OCT-1999 (first entry)			
DT	XX			
DB	XX			
XX	LU103 -specific amino acid consensus sequence.			
XX	IU103: amino acid; lung cancer; detection; FISH;			
KW	Fluorescent in situ hybridisation; protein.			
KW	(DIAD-) DIADEXUS LLC.			
OS	XX			
Synthetic.	XX			
Homo sapiens.	XX			
OS	OS			
PN	US5939265-A.			
PN	WPI: 1999-468402/39.			
PD	XX			
XX	PT			
XX	05-NOV-1997; 97US-00964725.			
PR	XX			
XX	05-NOV-1996; 96US-00744211.			
PA	XX			
(ABBO ) ABBOTT LAB.	PA			
XX	Friedman PN, Gordon J, Hodges SC, Cohen M, Kratochvil JD;			
PI	PI			
PI	Roberts-Rapp L, Russell JC, Stroupe SD, Klass MR;			
XX	XX			
DR	DR			
N-PSDB; AAX99-124.	DR			
XX	PT			
Polymerides useful for detecting, diagnosing and monitoring diseases	PT			
of the lung such as lung cancer.	PT			
XX	PS			
Claim 20; Col 53; 36PP; English.	PS			
XX	CC			
The 507 base pair sequence of a IU103 specific polymeride was derived	CC			
from a consensus of the isolated sequences from clones 1235095, 1235531	CC			
and 1379417. This sequence was then scanned for open reading frames. An	CC			
ORF was found and this polypeptide was produced. The polymerides and	CC			
methods are useful for detecting, diagnosing, staging, monitoring or	CC			
predicting diseases and conditions of the lung, such as lung cancer. The	CC			
polymerides may be used to produce probes for use in fluorescent in	CC			
situ hybridization (FISH) technology to perform chromosomal analysis and	CC			
identify cancer specific alterations such as deletions	CC			
XX	SQ	Sequence 93 AA;		
Query Match	100.0% ; Score 459; DB 2; Length 93;			
Best Local Similarity	100.0% ; Pred. No. 5.6e-47;			
Matches	93 ; Conservative 0 ; Mismatches 0 ; Indels 0 ; Gaps 0 ;			
		RESULT 4		
Qy	1 MKLVTIFLLTVTISCSYATAFLINKVLPVYDKLAPLPLDNILPFMDPKLKLTKLIGISV 60			
Db	1 MKLVTIFLLTVTISCSYATAFLINKVLPVYDKLAPLPLDNILPFMDPKLKLTKLIGISV 60			
		XX		
Qy	61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93			
Db	61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93			
		XX		
Qy	61 EHLVEGLRKCYNELGPEASEAVKKLEALSHLV 93			

KW	reproductive disorder; developmental disorder; arteriosclerosis;
KW	cirrhosis; Psoriasis; acquired immune deficiency syndrome; anemia;
KW	asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW	Parkinson's disease; Huntington's diseases; ovulatory defect;
KW	muscular dystrophy.
XX	
OS	<i>Homo sapiens</i> .
XX	
PN	WO200000610-A2.
XX	
PD	06-JAN-2000.
XX	
PP	25-JUN-1999;
XX	99MO-US014484.
PR	26-JUN-1998;
PR	98US-01090762P.
PR	31-JUL-1998;
PR	98US-01094983P.
PR	01-OCT-1998;
PR	98US-0102686P.
PR	11-DEC-1998;
XX	98US-0112129P.
DA	(TMCOY-) TMCOYDR PHARM TNC

L I N C - L I C E N S I N G   I N C.

XX Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baugh MR;  
 PI Alkerberd IE, Au-Yong J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;

XX DR WPII: 2000-160673/14.  
 DR N-PSDB; AAZ98174.

XX PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular  
 PR disease.

	CC	XX	SQ	Sequence 93 AA;
Query	Query	Match	100.0%	Score 459; DB 3; Length 93;
Best	Best	Local Similarity	100.0%	Pred. No. 5.6e-47;
Matches	Matches	93; Conservative	0; Mismatches 0;	Indels 0; Gaps 0;
Qy	1	MKLVTIFLVTISLSYSATAFLINKVPLPVDKLAPLDNLIPFMPLKLUKTIGISV	60	
Db	1	MKLVTIFLVTISLSYSATAFLINKVPLPVDKLAPLDNLIPFMPLKLUKTIGISV	60	
Qy	61	EHLVEGLRKCYNVELGPEASEAVKKLEALSHLV	93	
Db	61	EHLVEGLRKCYNVELGPEASEAVKKLEALSHLV	93	

RESULT 5  
AAU29145 standard; protein; 93 AA.  
ID AAU29145  
XX

presence of tumors, such as prostate and breast tumors, in mammals and to screen for modulators of the compounds.

PTT XX Claim 11; Fig 244; 774pp; English.

Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention. The PRO polypeptides and their associated nucleic acids can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of cells from the animal and a control sample of normal cells, whereby a higher level of expression in the test sample indicates the presence of a tumour in the mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats and rabbits but are preferably human. The polypeptides can be used to stimulate tumour necrosis factor (TNF) alpha release from human blood, when contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The PRO proteins can be used to determine the presence of tumours and also susceptibility to tumour development, particularly in the breast, prostate, rectal, cervical, or liver tumours, in mammalian subjects. The oligonucleotide probes specific for the PRO nucleic acids can be used for genetic analysis of individuals with genetic disorders.

XX SQ Sequence 93 AA;

Query Match	100.0%	Score 459;	DB 4;	Length 93;
Best Local Similarity	100.0%	Pred. No. 5	6e-0;	
Matches	93;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

```

Qy      1 MKLYTIPFLVITISLCSSATAFLINKVPDKLAPLDNLLPFMDPLKLUKTGTSV 60
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MKLYTIPFLVITISLCSSATAFLINKVPDKLAPLDNLLPFMDPLKLUKTGTSV 60
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy      61 EHIVVEGLRKCVNELGPSEASAEVKLLEALSHLV 93
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      61 EHIVVEGLRKCVNELGPSEASAEVKLLEALSHLV 93
       ||||| | | | | | | | | | | | | | | | | | | | | | | | | | |

```

#### RESULT 6

ID AB058521 standard; protein; 93 AA.  
XX  
AC AB058521;  
XX DT 15-APR-2003 (first entry)

XX Human PRO polypeptide #122.  
KW Human; PRO; cytosatic; tumour; cancer; breast; lung; stomach; liver;  
KW dog; cat; cow; horse; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.  
XX OS Homo sapiens.  
XX PN US2003027272-A1.  
XX PD 06-FEB-2003.  
XX PF 21-JUN-2003; 2002US-00176492.

XX PR 21-NOV-1997; 97US-0066120P.  
PR 24-NOV-1997; 97US-0066466P.  
PR 11-DEC-1997; 97US-0066772P.  
PR 12-DEC-1997; 97US-0069335P.  
PR 17-DEC-1997; 97US-0069425P.  
PR 18-DEC-1997; 97US-0069870P.  
PR 11-MAR-1998; 97US-0071450P.  
PR 11-MAR-1998; 98US-0077632P.  
PR 11-MAR-1998; 98US-0077649P.  
PR 20-MAR-1998; 98US-007886P.  
PR 20-MAR-1998; 98US-0079339P.  
PR 27-MAR-1998; 98US-0079664P.  
PR 27-MAR-1998; 98US-0079786P.  
PR 31-MAR-1998; 98US-0081195P.  
PR 31-MAR-1998; 98US-0081194P.  
PR 01-APR-1998; 98US-008327P.  
PR 01-APR-1998; 98US-008333P.  
PR 08-APR-1998; 98US-0083049P.  
PR 08-APR-1998; 98US-0084070P.  
PR 09-APR-1998; 98US-008195P.  
PR 15-APR-1998; 98US-0081838P.  
PR 21-APR-1998; 98US-0082568P.  
PR 22-APR-1998; 98US-008259P.  
PR 22-APR-1998; 98US-0082197P.  
PR 28-APR-1998; 98US-0083312P.  
PR 28-APR-1998; 98US-0083495P.  
PR 29-APR-1998; 98US-0083496P.  
PR 29-APR-1998; 98US-0083499P.  
PR 29-APR-1998; 98US-0083559P.  
PR 05-MAY-1998; 98US-008436P.  
PR 05-MAY-1998; 98US-008441P.  
PR 07-MAY-1998; 98US-008463P.  
PR 07-MAY-1998; 98US-0084640P.  
PR 07-MAY-1998; 98US-0084643P.  
PR 15-MAY-1998; 98US-0085579P.  
PR 15-MAY-1998; 98US-0085580P.  
PR 15-MAY-1998; 98US-0085582P.  
PR 15-MAY-1998; 98US-0085700P.  
PR 18-MAY-1998; 98US-0086023P.  
PR 22-MAY-1998; 98US-0086392P.  
PR 22-MAY-1998; 98US-0086486P.  
PR 28-MAY-1998; 98US-0087098P.  
PR 28-MAY-1998; 98US-0087208P.  
PR 28-MAY-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088863P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-008909P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-008912P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089538P.

PR	23-SEP-1998;	98US-010175P.
PR	23-SEP-1998;	98US-0101477P.
PR	24-SEP-1998;	97US-0101238P.
PR	24-SEP-1998;	98US-0101739P.
PR	24-SEP-1998;	98US-0101443P.
PR	24-SEP-1998;	98US-0101922P.
PR	25-SEP-1998;	98US-0101786P.
PR	29-SEP-1998;	98US-0102207P.
PR	29-SEP-1998;	98US-010240P.
PR	29-SEP-1998;	98US-0102310P.
PR	29-SEP-1998;	98US-0102311P.
PR	30-SEP-1998;	98US-010248P.
PR	30-SEP-1998;	98US-0102570P.
PR	30-SEP-1998;	98US-0102571P.
PR	01-OCT-1998;	98US-0102684P.
PR	01-OCT-1998;	98US-0102687P.
PR	02-OCT-1998;	98US-0102965P.
PR	06-OCT-1998;	98US-0103298P.
PR	06-OCT-1998;	98US-0103459P.
PR	07-OCT-1998;	98US-00168978.
Query Match Score 459; DB 6; Length 93;		
Best Local Similarity 100.0%; Pred. No. 5.6e-47;		
Matches 93; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	1 MKLVTFILVTTISCSYSATAFLINKVLPVDKGLAPLPLDNTLPMDPLKLKLTGIGSV 60	
Db	1 MKLVTFILVTTISCSYSATAFLINKVLPVDKGLAPLPLDNTLPMDPLKLKLTGIGSV 60	
Qy	61 EHLYVGLRKCVNELGPSEAVKLLKEALSHLY 93	
Db	61 EHLYVGLRKCVNELGPSEAVKLLKEALSHLY 93	
RESULT 7		
ABU8069 Standard; protein; 93 AA.		
ID	ABU8069	
XX		
AC		
XX		
DT	07-JUL-2003 (first entry)	
XX		
DE	Novel human secreted and transmembrane protein PRO1128.	
XX		
KW	Human; secreted and transmembrane protein; PRO; gene therapy;	
KW	tumour necrosis factor-alpha release; TNF-alpha release;	
KW	chondrocyte proliferation; chondrocyte differentiation; tumour;	
KW	adrenal tumour; lung tumour; colon tumour; breast tumour;	
KW	prostate tumour; rectal tumour; cervical tumour; liver tumour.	
XX		
OS	Homo sapiens.	
XX		
PN	US2003032127-A1.	
XX		
PD	13-FEB-2003.	
XX		
PP	26-JUN-2002; 2002US-00183012.	
XX		
PR	18-SEP-1997;	97US-0059263P.
PR	18-SEP-1997;	97US-0062250P.
PR	17-OCT-1997;	97US-0059266P.
PR	21-OCT-1997;	97US-0106486P.
PR	24-OCT-1997;	97US-0063120P.
PR	24-OCT-1997;	97US-0063121P.
PR	28-OCT-1997;	97US-0063340P.
PR	28-OCT-1997;	97US-0063541P.
PR	28-OCT-1997;	97US-0063544P.
PR	28-OCT-1997;	97US-0063545P.
PR	29-OCT-1997;	97US-0063734P.
PR	31-OCT-1997;	97US-0063810P.
PR	31-OCT-1997;	97US-0064103P.
PR	13-NOV-1997;	97US-0065311P.
PR	21-NOV-1997;	97US-0065120P.
PR	21-NOV-1997;	97US-0065120P.

PR	24-NOV-1997;	97US-0066466P.	98US-0089653P.
R	24-NOV-1997;	97US-0066712P.	98US-0089308P.
R	11-DEC-1997;	97US-006935P.	98US-0089522P.
R	12-DEC-1997;	97US-006945P.	98US-0090246P.
R	17-DEC-1997;	97US-0069870P.	98US-0090549P.
R	18-DEC-1997;	97US-0068017P.	98US-0090429P.
R	10-MAR-1998;	98US-0077450P.	98US-0090415P.
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R	11-MAR-1998;	98US-0077649P.	98US-0090461P.
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XX	KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing.	
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XX	KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy; tissue typing.	
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 AC ABR66258;  
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 XX DE Human secreted polypeptide PRO1128, SEQ ID NO:244.  
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 KW Homo sapiens.  
 OS XX  
 XX US2003027278-AL.  
 PN XX  
 XX PD 06-FEB-2003.  
 XX PF 21-JUN-2002; 2002US-00176987.  
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**RESULT 10**  
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 XX bone disorder; arthritis; sports injury; cancer; tumour; diagnosis;  
 XX adrenal tumour; lung; colon; breast; prostate; kidney; rectum; cervix;  
 XX liver; drug screening; transgenic animal; genetic analysis;  
 XX antiarthritis; vulnereity; gene therapy.  
 XX Homo sapiens.  
 XX US2003036159-A1.  
 XX 20-FEB-2003.  
 PF 02-JUL-2002; 2002US-00188773.  
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 ID ABU9588 standard; protein; 93 AA.  
 DT 09-AUG-2003 (first entry)  
 XX DE Human secreted/transmembrane protein (PRO) #122.  
 XX KW tumour necrosis factor alpha; chondrocyte cell; tumour; gene therapy;  
 XX KW tissue typing.  
 XX OS Homo sapiens.  
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 XX PR 27-FEB-2003.  
 XX PR 27-ITN-2002; 2002US-00184627.  
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ID ABU89948

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AC ABU89948;

DT 11-AUG-2003 (first entry)

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Human; gene therapy; tissue typing; tumour; chondrocyte proliferation; chondrocyte differentiation; tumour necrosis factor-alpha release; affinity purification.

Homo sapiens.

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